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(54) Title: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE

**(57) Abstract**

Compounds and methods for treating prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of prostate cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides.

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COMPOUNDS FOR IMMUNOTHERAPY  
OF PROSTATE CANCER AND METHODS FOR THEIR USE

TECHNICAL FIELD

The present invention relates generally to compositions and methods for the treatment of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein and to DNA molecules encoding such polypeptides. Such polypeptides may be used in vaccines and pharmaceutical compositions for treatment of prostate cancer.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved vaccines and treatment methods for prostate cancer.

## SUMMARY OF THE INVENTION

The present invention provides compounds and methods for immunotherapy of prostate cancer. In one aspect, polypeptides are provided comprising at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants thereof.

In related aspects, DNA molecules encoding the above polypeptides are provided. In specific embodiments, such DNA molecules include sequences provided in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224. The present invention further provides expression vectors comprising the above DNA molecules and host cells transformed or transfected with such expression vectors. In preferred embodiments, the host cells are selected from the group consisting of *E. coli*, yeast and mammalian cells.

In another aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, an inventive polypeptide and a known prostate antigen.

The present invention also provides pharmaceutical compositions comprising one or more of the above polypeptides, or a DNA molecule encoding such polypeptides, and a physiologically acceptable carrier, together with vaccines comprising one or more of such polypeptide or DNA molecules in combination with a non-specific immune response enhancer.

In related aspects, pharmaceutical compositions for the treatment of prostate cancer comprising one or more polypeptides and a physiologically acceptable carrier are provided, wherein the polypeptide comprises an immunogenic portion of a prostate tumor protein or of a variant of said protein that differs only in conservative substitutions and/or modifications, the prostate tumor protein being encoded by a DNA molecule having a

sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants thereof. The invention also provides vaccines for the treatment of prostate cancer comprising such polypeptides in combination with a non-specific immune response enhancer, together with pharmaceutical compositions and vaccines comprising one or more DNA molecules having a sequence provided in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221. Pharmaceutical compositions and vaccines comprising one or more of the above fusion proteins are also provided.

In yet another aspect, methods are provided for inhibiting the development of prostate cancer in a patient, comprising administering an effective amount of at least one of the above pharmaceutical compositions and/or vaccines.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

#### DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunotherapy of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant of such a protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-

65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 181, 188, 191, 193, 194, 198, 203, 204, and 207-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, <sup>125</sup>I-labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of

one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recited nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers

to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a

growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain preferred embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end

of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may generally be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the

immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or fusion proteins comprising one or more such polypeptides and/or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides (or fusion proteins or DNA molecules encoding such polypeptides) may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide or fusion protein is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (e.g., polylactic galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (*i.e.*, a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the

use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (i.e., untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1  $\mu$ g. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary

depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATE<sup>TM</sup> system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

Polypeptides of the present invention may also, or alternatively, be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of one or more of the

above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about  $10^3$  L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10  $\mu$ g, and preferably about 100 ng to about 1  $\mu$ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20<sup>TM</sup> (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20<sup>TM</sup>. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1  $\mu$ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include <sup>90</sup>Y, <sup>123</sup>I, <sup>125</sup>I, <sup>131</sup>I, <sup>186</sup>Re, <sup>188</sup>Re, <sup>211</sup>At, and <sup>212</sup>Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulphydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulphydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitzer), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis *et al. Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

The following Examples are offered by way of illustration and not by way of limitation.

### EXAMPLES

#### Example 1

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A<sup>+</sup> RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A<sup>+</sup> RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor

library contained  $1.64 \times 10^7$  independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained  $3.3 \times 10^6$  independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70  $\mu$ g) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100  $\mu$ l of H<sub>2</sub>O, heat-denatured and mixed with 100  $\mu$ l (100  $\mu$ g) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50  $\mu$ l) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23  $\mu$ l H<sub>2</sub>O to form the driver DNA.

To form the tracer DNA, 10  $\mu$ g prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5  $\mu$ l H<sub>2</sub>O. Tracer DNA was mixed with 15  $\mu$ l driver DNA and 20  $\mu$ l of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12  $\mu$ l H<sub>2</sub>O, mixed with 8  $\mu$ l driver DNA and 20  $\mu$ l of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into

BamHI/XbaI site of chloramphenicol resistant pBCSK<sup>+</sup> (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (prostate subtraction 1).

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1  $\mu$ g each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was

performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are

provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS:

93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively. cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

## Example 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR  
POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2  $\mu$ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR,  $\beta$ -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using  $\beta$ -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the  $\beta$ -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the  $\beta$ -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in

prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal

colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

### Example 3

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no

significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

#### Example 4

#### SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANTS: Xu, Jiangchun  
Dillin, Davin C.
- (ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE
- (iii) NUMBER OF SEQUENCES: 224
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: SEED and BERRY LLP
  - (B) STREET: 6300 Columbia Center, 701 Fifth Avenue
  - (C) CITY: Seattle
  - (D) STATE: WA
  - (E) COUNTRY: USA
  - (F) ZIP: 98104
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 23-FEB-1998
  - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Maki, David J.
  - (B) REGISTRATION NUMBER: 31,392
  - (C) REFERENCE/DOCKET NUMBER: 210121.427C3
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (206) 622-4900
  - (B) TELEFAX: (206) 682-6031

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 814 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT TTTTCACAG TATAACAGCT CTTTATTCT GTGAGTTCTA CTAGGAAATC	60
ATCAAATCTG AGGGTTGTCT GGAGGACTTC AATACACCTC CCCCCATAGT GAATCAGCTT	120
CCAGGGGGTC CAGTCCCTCT CCTTACTTCA TCCCCATCCC ATGCCAAAGG AAGACCCCTCC	180
CTCCTTGGCT CACAGCCTTC TCTAGGCTTC CCAGTGCTC CAGGACAGAG TGGGTTATGT	240
TTTCAGCTCC ATCCTTGCTG TGAGTGTCTG GTGCGTTGTG CCTCCAGCTT CTGCTCAGTG	300
CTTCATGGAC AGTGTCCAGC ACATGTCACT CTCCACTCTC TCAGTGTGGA TCCACTAGTT	360
CTAGAGCGGC CGCCACCGCG GTGGAGCTCC AGCTTTGTT CCCTTTAGTG AGGGTTAATT	420

GCAGCGCTTGG CGTAATCATG GTCATAACTG TTTCTGTGT GAAATTGTTA TCCGCTCACA	480
ATTCCACACA ACATACGAGC CGGAAGCATA AAGTGTAAAG CCTGGGGTGC CTAATGAGTG	540
ANCTAACTCA CATTAATTGC GTTGCCTCA CTGNCCGCTT TCCAGTCNNG AAAACTGTCG	600
TGCCAGCTGC ATTAATGAAT CGGCCAACGC NCAGGGAAAA GCGGTTGCG TTTTGGGGC	660
TCTTCGCTT CTCGCTCACT NANTCCTGCG CTCGGTCNTT CGGCTGCGG GAACGGTATC	720
ACTCCTCAAA GGNGGTATTA CGGTTATCCN NAAATCNGGG GATAACCCNGG AAAAAANTTT	780
AACAAAAGGG CANCAAAGGG CNGAAACGTA AAAA	814

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACAGAAATGT TGGATGGTGG AGCACCTTTC TATACGACTT ACAGGACAGC AGATGGGAA	60
TTCATGGCTG TTGGAGCAAT AGAACCCAG TTCTACGAGC TGCTGATCAA AGGACTTGGA	120
CTAAAGTCTG ATGAACTTCC CAATCAGATG AGCATGGATG ATTGGCCAGA AATGAAGAAG	180
AAGTTTGCAG ATGTATTTGC AAAGAAGACG AAGGCAGAGT GGTGTCAAAT CTTTGACGGC	240
ACAGATGCCT GTGTGACTCC GGTCTGACT TTTGAGGAGG TTGTTCATCA TGATCACAAC	300
AAGGAACGGG GCTCGTTAT CACCAAGTGGAG GAGCAGGACG TGAGCCCCCG CCCTGCACCT	360
CTGCTGTTAA ACACCCCAGC CATCCCTTCT TTCAAAAGGG ATCCACTAGT TCTAGAAGCG	420
GCCGCCACCG CGGTGGAGCT CCAGCTTTG TTCCCTTAG TGAGGGTTAA TTGCGCGCTT	480
GGCGTAATCA TGGTCATAGC TGTTTCTGT GTGAAATTGT TATCCGCTCA CAATTCCCCC	540
AACATACGAG CCGGAACATA AAGTGTAAAG CCTGGGGTGC CTAATGANTG AGCTAACTCN	600
CATTAATTGC GTTGCCTCA CTGCCGCTT TCCAGTCGGG AAAACTGTCG TGCCACTGCN	660
TTANTGAATC NGCCACCCCC CGGGAAAAGG CGGTTGCNTT TTGGGCCTCT TCCGCTTCC	720
TCGCTCATCG ATCCTNGCNC CCGGTCTTCG GCTGCGGNGA ACGGTTCACT CCTCAAAGGC	780
GGTNTNCCGG TTATCCCCAA ACNGGGATA CCCNGA	816

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTTTGAAAG AAGGGATGGC TGGGGTGTTC AACAGCAGAG GTGCAGGGCG GGGGCTCACG	60
TCCTGCTCCT CACTGGTGAT AAACGAGCCC CGTTCTTGT TGTGATCATG ATGAACAAACC	120
TCCTCAAAAG TCAGAACCGG AGTCACACAG GCATCTGTGC CGTCAAAGAT TTGACACCAC	180
TCTGCCTTCG TCTTCTTTGC AAATACATCT GCAAACCTCT TCTTCATTTC TGGCAATCA	240
TCCATGCTCA TCTGATTGGG AAGTTCATCA GACTTTAGTC CANNTCTTT GATCAGCAGC	300
TCGTAGAACT GGGGTTCTAT TGCTCCAACA GCCATGAATT CCCCATCTGC TGTCTGTAA	360
GTCGTATAGA AAGGTGCTCC ACCATCCAAC ATGTTCTGTC CTCGAGGGGG GGCCCGGTAC	420
CCAATTGCGC CTATANTGAG TCGTATTACG CGCGCTCACT GGCGCTCGTT TTACAAAGTC	480
GTGACTGGGA AAACCCCTGGG CGTTACCAAC TTAATCGCCT TGCAGCACAT CCCCCTTCG	540
CCAGCTGGGC GTAATANCAGA AAAGGCCGC ACCGATCGCC CTTCCAACAG TTGCGCACCT	600
GAATGGGNAA ATGGGACCCC CCTGTTACCG CGCATTNAAC CCCCAGGGG TTTNGTTGTT	660
ACCCCCACNT NNACCGCTTA CACTTTGCCA GCGCCTTANC GCCCCTCCC TTTCNCTTT	720
CTTCCCTTCC TTTCNCCCN CTTTCCCCCG GGGTTCCCC CNTCAAACCC CNA	773

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTCCTGAGT CCTACTGACC	TGTGCTTCT GGTGTGGAGT	CCAGGGCTGC	TAGGAAAAGG	60
AATGGGCAGA CACAGGTGTA	TGCCAATGTT TCTGAAATGG	GTATAATTTC	GTCCTCTCCT	120
TCGGAACACT GGCTGTCTCT	GAAGACTTCT	CGCTCAGTTT	CAGTGAGGAC	180
ACGTGGGTGA CCATGTTGTT	TGTGGGGTGC	AGAGATGGGA	GGGGTGGGGC	240
AGAGTGGACA GTGACACAAG	GTGGACACTC	TCTACAGATC	ACTGAGGATA	300
ACAATGCATG AGGCACACAC	ACAGCAAGGA	TGACNCTGTA	AACATAGCCC	360
GNGGGCACTG GGAAGCCTAN	ATNAGGCCGT	GAGCANAAAG	AAGGGGAGGA	420
CTANAGCGGC CGCCACCGCG	GTGGANCTCC	ANCTTTGTT	CCCTTAGTG	480
GCGCGCTTGG CNTAACATG	GTCATANCTN	TTTCCTGTGT	GAAATTGTTA	540
ATTCCACACA ACATACGANC	CGGAAACATA	AANTGTAAAC	CTGGGGTGCC	600
CTAACTCACA TTAATTGCGT	TGCGCTCACT	GCCCCTTTC	TAATGANTGA	660
CCNCTTGCAT TNATGAATCN	GCCAACCCCC	CAATCNGGAA	ACCTGTCTTG	720
TCCGCTTCCT CNCTCANTTA	NTCCCTNCNC	TCGGTCATTC	TGGCTGCNGC	780
ACCNCTCCA AAGGGGTAT	TCCGGTTTCC	CCNAATCCGG	AAACCGGTTTC	
				828

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTTTTT TTTTTACTGA	TAGATGGAAT TTATTAAGCT	TTTCACATGT	GATAGCACAT	60
AGTTTTAATT GCATCAAAG	TACTAACAAA	AACTCTAGCA	ATCAAGAATG	120
ATTTTATAAC AATCAACACC	TGTGGCTTTT	AAAATTGTT	TTTCATAAGA	180
TGAAGTAAAT CTAGCCATGC	TTTAAAAAAA	TGCTTTAGGT	CACTCCAAGC	240
ACATTGGCA TAAACAATAA	TAAAACAATC	ACAATTAAAT	AAATAACAAA	300
TAGGCCATAA TCATATACAG	TATAAGGAAA	AGGTGGTAGT	GTTGAGTAAG	360
AATAGAATAC CTTGGCTCT	ATGCAAATAT	GTCTAGACAC	TTTGATTAC	420
CATTCAAGTT TCAAAGTAGG	AGACAGGTT	TACAGTATCA	TTTTACAGTT	480
TGAAAACAAG TAGAAAATGA	TGAGTTGATT	TTTATTAATG	CATTACATCC	540
TCACCAAACCC CTCAGTTATA	AAAAATTTC	AAGTTATATT	AGTCATATAA	600
TTATTTAAA TTAGTGCTAA	ATGGATTAAG	TGAAGACAAC	AATGGTCCCC	660
GATATTGGTC ATTTTACCA	GCTTCTAAAT	CTNAACTTTC	AGGCTTTGA	720
TGNATNACAG TGTCCANAG	TTNCAACCTA	CTGGAACATT	ACTGGAACAT	780
TGTTATTTG TTAAAAATTA	AATTTAACC	ACAGTGTGCT	TGATTCAAAA	
				834

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTTT	TTTTTTTTTT	AAGACCTCA	TCAATAGATG	GAGACATACA	GAAATAGTCA	60
AACCACATCT	ACAAAATGCC	AGTATCAGGC	GGCGGCTTCG	AAGCCAAAGT	GATGTTGGA	120
TGTAAAGTGA	AATATTAGTT	GGCGGATGAA	GCAGATAGTG	AGGAAAGTTG	AGCCAATAAT	180
GACGTGAAGT	CCGTGGAAGC	CTGTGGCTAC	AAAAAAATGTT	GAGCCGTAGA	TGCCGTGGA	240
AATGGTGAAG	GGAGACTCGA	AGTACTCTGA	GGCTTGTAGG	AGGGTAAAAT	AGAGACCCAG	300
TAAAATTGTA	ATAAGCAGTG	CTTGAATTAT	TTGGTTTCGG	TTGTTTCTA	TTAGACTATG	360
GTGAGCTCAG	GTGATTGATA	CTCCTGATGC	GAGTAATACG	GATGTGTTA	GGAGTGGGAC	420
TTCTAGGGGA	TTTAGCGGGG	TGATGCCTGT	TGGGGGCCAG	TGCCCTCCTA	GTTGGGGGTT	480
AGGGGCTAGG	CTGGAGTGGT	AAAAGGCTCA	GAAAAATCCT	GCGAAGAAAA	AAACTTCTGA	540
GGTAATAAAT	AGGATTATCC	CGTATCGAAG	GCCTTTTGG	ACAGGTGGTG	TGTGGTGGCC	600
TTGGTATGTG	CTTTCTCGTG	TTACATCGCG	CCATCATTGG	TATATGGTTA	GTGTGTTGGG	660
TTANTANGGC	CTANTATGAA	GAACCTTTGG	ANTGGAATTA	AATCAATNGC	TTGGCCGGAA	720
GTCATTANGA	NGGCTNAAAA	GGCCCTGTTA	NGGGTCTGGG	CTNGGTTTA	CCCNACCCAT	780
GGAATNCNCC	CCCCGGACNA	NTGNATCCCT	ATTCTTAA			818

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTTTT	TTTTTTTTTT	TGGCTCTAGA	GGGGTAGAG	GGGGTGCAT	AGGGTAAATA	60
CGGGCCCTAT	TTCAAAGATT	TTTAGGGAA	TTAATTCTAG	GACGATGGGT	ATGAAACTGT	120
GGTTTGCCTC	ACAGATTCA	GAGCATTGAC	CGTAGTATAC	CCCCGGTCGT	GTAGCGGTGA	180
AAGTGGTTG	GTTCAGACGT	CCGGGAATTG	CATCTGTTT	TAAGCCTAAT	GTGGGGACAG	240
CTCATGAGTG	CAAGACGTCT	TGTGATGTAA	TTATTATACN	AATGGGGCT	TCAATCGGA	300
GTACTACTCG	ATTGTCAACG	TCAAGGAGTC	GCAGGTCGCC	TGGTTCTAGG	AATAATGGGG	360
GAAGTATGTA	GGAATTGAAG	ATTAATCCGC	CGTAGTCGGT	GTTCTCCTAG	GTTCAATACC	420
ATTGGTGGCC	AATTGATTG	ATGGTAAGGG	GAGGGATCGT	TGAACTCGTC	TGTTATGTAA	480
AGGATNCCTT	NGGGATGGGA	AGGCNATNAA	GGACTANGGA	TNAATGGCGG	GCANGATATT	540
TCAAACNGTC	TCTANTTCCT	GAAACGTCTG	AAATGTTAAT	AANAATTAAN	TTTNGTTATT	600
GAATNTTNNG	AAAAAGGGCT	TACAGGACTA	GAAACCAAAT	ANGAAAANTA	ATNNTAANGG	660
CNTTATCNTN	AAAGGTNATA	ACCNCCTCTA	TNATCCCACC	CAATNGNATT	CCCCACNCNN	720
ACNATTGGAT	NCCCCANTTC	CANAAANGGC	CNCCCCCGG	TGNANNCCNC	CTTTGTTCC	780
CTTNANTGAN	GGTTATTNC	CCCTNGCNTT	ATCANCC			817

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATTTCCGGG	TTTACTTTCT	AAGGAAAGCC	GAGCGGAAGC	TGCTAACGTG	GGAATCGGTG	60
CATAAGGAGA	ACTTTCTGCT	GGCACGCGCT	AGGGACAAGC	GGGAGAGCGA	CTCCGAGCGT	120

CTGAAGCGCA	CGTCCCAGAA	GGTGGACTTG	GCACTGAAAC	AGCTGGGACA	CATCCGGAG	180
TACGAACAGC	GCCTGAAAGT	GCTGGAGCGG	GAGGTCAGC	AGTGTAGCCG	CGTCCTGGG	240
TGGGTGGCCG	ANGCCTGANC	CGCTCTGCCT	TGCTGCC	ANGTGGGCCG	CCACCCCTG	300
ACCTGCCTGG	GTCCAAACAC	TGAGCCCTGC	TGGCGGACTT	CAAGGANAAC	CCCCACANGG	360
GGATTTGCT	CCTANANTAA	GGCTCATCTG	GGCCTCGGCC	CCCCCACCTG	GTTGGCCTTG	420
TCTTGANGT	GAGCCCCATG	TCCATCTGGG	CCACTGTCNG	GACCACCTT	NGGGAGTGTT	480
CTCCTTACAA	CCACANNATG	CCCGGCTCCT	CCCGGAAACC	ANTCCCANCC	TGNGAAGGAT	540
CAAGNCCTGN	ATCCACTNNT	NCTANAACCG	GCCNCNC	CNGTGGAAC	CNCCTTNTGT	600
TCCTTTCTNT	TNAGGGTTAA	TNNCGCCTTG	GCCTTNCCAN	NGTCCTNCNC	NTTTTCCNNT	660
GTTNAAATTG	TTANGCNCC	NCCNNTCCCN	CNNCN	CNNAN	CCCGACCCNN	720
NCCTGGGGGT	NCCNNNGAT	TGACCCNNCC	NCCNTNTANT	TGCNTTNGG	NNCNNTGCC	780
CTTCCCTCT	NGGGANNCG					799

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 801 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCCTTGAT	CCTCCCAGGC	TGGGACTGGT	TCTGGGAGGA	GCCGGGCATG	CTGTGGTTG	60
TAANGATGAC	ACTCCAAAG	GTGGTCTGA	CAGTGGCCCA	GATGGACATG	GGGCTCACCT	120
CAAGGACAAG	GCCACCAGGT	GCGGGGGCCG	AAGCCCACAT	GATCCTTA	CTATGAGCAA	180
AATCCCCTGT	GGGGGCTTCT	CCTTGAAGTC	CGCCANCAGG	GTCAGTCTT	TGGACCCANG	240
CAGGTCA	GGTTGTNGNC	CAACTGGGGG	CCNCAACGCA	AAANGCNCA	GGGCCTCNGN	300
CACCCATCCC	ANGACCGGGC	TACACTNCTG	GACCTCCNC	TCCACCAC	TCATGCGCTG	360
TTCNTACCCG	CGNATNTGTC	CCANCTGTT	CNGTGCNAC	TCCAN	NGGACGTGCG	420
CTACATACGC	CCGGANTCNC	NCTCCGCTT	TGTCCCTATC	CACGTNCCAN	CAACAAATT	480
CNCCNTANTG	CACCNATTCC	CACNTTNNC	AGNTTCCNC	NNCGNGCTTC	CTTNTAAAAG	540
GGTTGANCCC	CGGAAAATNC	CCCAAAGGGG	GGGGGCCNGG	TACCCAAC	CCCCCTNATA	600
GCTGAANTCC	CCATNACNN	GNCTNATGG	ANCCNTCCNT	TTTAANNACN	TTCTNAACTT	660
GGGAANANCC	CTCGNCCNTN	CCCCN	TCCCN	CNANGNN	CCCCNNTCC	720
NCCCNNTNG	GCNTNTNANN	CNAAAAGGC	CCNNN	ANCAA	TCTC	780
CCANCCCTCG	AAATCGGCCN	C				801

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 789 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGTCTATNT	GGCCAGTGTG	GCAGCTTCC	CTGTGGCTGC	CGGTGCCACA	TGCCTGTCCC	60
ACAGTGTGGC	CGTGGTGACA	GCTTCAGCCG	CCCTCACCGG	GTTCACCTTC	TCAGCCCTGC	120
AGATCCTGCC	CTACACACTG	GCCTCCCTCT	ACCACCGGGA	GAAGCAGGTG	TTCTGCCCCA	180
AATACCGAGG	GGACACTGGA	GGTGTAGCA	GTGAGGACAG	CCTGATGACC	AGCTTCCTGC	240
CAGGCCCTAA	GCCTGGAGCT	CCCTTCCCTA	ATGGACACGT	GGGTGCTGGA	GGCAGTGGCC	300
TGCTCCCACC	TCCACCCGCG	CTCTGCGGGG	CCTCTGCCTG	TGATGTCTCC	GTACGTGTGG	360
TGGTGGGTGA	GCCCACCGAN	GCCAGGGTGG	TTCCGGGCCG	GGGCATCTGC	CTGGACCTCG	420
CCATCCTGGA	TAGTGCTTCC	TGCTGTCCA	NGTGGCCCCA	TCCCTGTTA	TGGGCTCCAT	480
TGTCCAGCTC	AGCCAGTCTG	TCACTGCCA	TATGGTGTCT	GCCGCAGGCC	TGGGTCTGGT	540

CCCATTTACT TTGCTACACA GGTANTATT GACAAGAACG ANTTGGCCAA ATACTCAGCG	600
TTAAAAAATT CCAGCAACAT TGGGGGTGGA AGGCCTGCCT CACTGGGTCC AACTCCCCGC	660
TCCTGTTAAC CCCATGGGC TGCCGGCTTG GCCGCCAATT TCTGTTGCTG CCAAANTNAT	720
GTGGCTCTCT GCTGCCACCT GTTGCTGGCT GAAGTGCNTA CNGNCANCT NGGGGGGTNG	780
GGNGTTCCC	789

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 772 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCACCCCTAC CCAAATATTAA GACACCAACA CAGAAAAGCT AGCAATGGAT TCCCTTCTAC	60
TTTGTAAAT AAATAAGTTA AATATTAAA TGCCTGTGTC TCTGTGATGG CAACAGAAGG	120
ACCAACAGGC CACATCCTGA TAAAAGGTA GAGGGGGGTG GATCAGCAAA AAGACAGTGC	180
TGTGGGCTGA GGGGACCTGG TTCTTGTGTG TTGCCCCCTCA GGACTCTTCC CCTACAAATA	240
ACTTTCATAT GTTCAAATCC CATGGAGGAG TGTTTCATCC TAGAAACTCC CATGCAAGAG	300
CTACATTAAA CGAAGCTGCA GGTAAAGGGG CTTANAGATG GGAAACCAGG TGACTGAGTT	360
TATTCAGCTC CCAAAAACCC TTCTCTAGGT GTGTCTCAAC TAGGAGGCTA GCTGTTAAC	420
CTGAGCCTGG GTAATCCACC TGCAGAGTCC CCGCATTCCA GTGCATGGAA CCCTTCTGGC	480
CTCCCTGTAT AAGTCCAGAC TGAAACCCCC TTGGAAGGNC TCCAGTCAGG CAGCCCTANA	540
AACTGGGGAA AAAAGAAAAG GACGCCCAN CCCCCAGCTG TGCANCTACG CACCTCAACA	600
GCACAGGGTG GCAGCAAAAA AACCACTTTA CTTTGGCACA AACAAAAACT NGGGGGGGCA	660
ACCCCGGCAC CCCNANGGG GTTAACAGGA ANCNGGGNAA CNTGGAACCC AATTNAGGCA	720
GGCCCNCCAC CCCNAATNTT GCTGGAAAT TTTCTCTCCC CTAAATTNTT TC	772

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 751 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCCCAATTC CAGCTGCCAC ACCACCCACG GTGACTGCAT TAGTTGGAT GTCATACAAA	60
AGCTGATTGA AGCAACCCTC TACTTTTG TGCGTGCCT TTTGCTTGGT GCAGGTTCA	120
TTGGCTGTGT TGGTGACGTT GTCATTGCAA CAGAATGGGG GAAAGGCAGT GTTCTCTTG	180
AAGTANGGTG AGTCCTCAAA ATCCGTATAG TTGGTGAAGC CACAGCACTT GAGCCCTTC	240
ATGGTGGTGT TCCACACTTG AGTGAAGTCT TCCTGGAAC CATAATCTT CTTGATGGCA	300
GGCACTACCA GCAACGTCAG GGAAGTGCTC AGCCATTGTG GTGTACACCA AGGCGACCAC	360
AGCAGCTGCN ACCTCAGCAA TGAAGATGAN GAGGANGATG AAGAAGAACG TCNCGAGGGC	420
ACACTTGCTC TCAGTCTTAN CACCATANCA GCCCNTGAAA ACCAANANCA AAGACCACNA	480
CNCCGGCTGC GATGAAGAAA TNACCCNCG TTGACAAACT TGCATGGCAC TGGGANCCAC	540
AGTGGCCCNA AAAATCTTCA AAAAGGATGC CCCATCNATT GACCCCCCAA ATGCCCACTG	600
CCAACAGGGG CTGCCCCACN CNCNNAACGA TGANCCNATT GNACAAAGATC TNCNTGGTCT	660
TNATNAACNT GAACCCCTGCN TNGTGGCTCC TGTTCAAGGNC CNNGGCCTGA CTTCTNAANN	720
AANGAACTCN GAAGNCCCCA CNGGANANN G	751

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCAGGCG	TCCCTCTGCC	TGCCCACTCA	GTGGCAACAC	CCGGGAGCTG	TTTGTCTT	60
TGTGGANCCT	CAGCAGTNCC	CTCTTTCAGA	ACTCANTGCC	AAGANCCCTG	AACAGGAGCC	120
ACCATGCAGT	GCTTCAGCTT	CATTAAGACC	ATGATGATCC	TCTTCATTT	GCTCATCTT	180
CTGTGTGGTG	CAGCCCTGTT	GGCAGTGGGC	ATCTGGGTGT	CAATCGATGG	GGCATCCTT	240
CTGAAGATCT	TCGGGCCACT	GTCGTCCAGT	GCCATGCAGT	TTGTCAACGT	GGGCTACTTC	300
CTCATCGCAG	CCGGCGTTGT	GGTCTTAGCT	CTAGGTTTCC	TGGGCTGCTA	TGGTGCTAAG	360
ACTGAGAGCA	AGTGTGCCCT	CGTGACGTTC	TTCTTCATCC	TCCTCCTCAT	CTTCATTGCT	420
GAGGTTGCAA	TGCTGTGGTC	GCCTTGGTGT	ACACCCAAAT	GGCTGAGCAC	TTCCTGACGT	480
TGCTGGTAAT	GCCTGCCATC	AANAAAAGAT	TATGGGTTCC	CAGGAANACT	TCACTCAAGT	540
GTTGGAACAC	CACCATGAAA	GGGCTCAAGT	GCTGTGGCTT	CNNCCAACTA	TACGGATTT	600
GAAGANTCAC	CTACTTCAAA	AAAAANAGTG	CCTTCCCCC	ATTTCTGTTG	CAATTGACAA	660
ACGTCCCCAA	CACAGCCAAT	TGAAAACCTG	CACCCAACCC	AAANGGTCC	CCAACCANAA	720
					ATTNAAGGG	729

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCTTCCT	CAAAGTTGTT	CTTGTGCCA	TAACAACCAC	CATAGGTAAA	GCGGGCGCAG	60
TGTCGCTGA	AGGGGTTGTA	GTACCAGCGC	GGGATGCTCT	CCTTGAGAG	TCCTGTGTCT	120
GGCAGGTCCA	CGCAGTGCC	TTTGTCACTG	GGGAAATGGA	TGCGCTGGAG	CTCGTCAAAG	180
CCACTCGTGT	ATTTTCACA	GGCAGCCTCG	TCCGACCGT	CGGGGCAGTT	GGGGGTGTCT	240
TCACACTCCA	GGAAACTGTC	NATGCAGCAG	CCATTGCTGC	AGCGGAACGT	GGTGGGCTGA	300
CANGTGCCAG	AGCACACTGG	ATGGCGCCTT	TCCATGNAN	GGGCCCTGNG	GGAAAGTCCC	360
TGANCCCCAN	ANCTGCCTCT	CAAANGCCCC	ACCTTGACACA	CCCCGACAGG	CTAGAATGGA	420
ATCTTCTTCC	CGAAAGGTAG	TTNTTCTTGT	TGCCCAANCC	ANCCCCNTAA	ACAAACTCTT	480
GCANATCTGC	TCCGNGGGG	TCNTANTACC	ANC GTGGAA	AAGAACCCCA	GGCNGCGAAC	540
CAANCTTGTT	TGGATNCGAA	GCNATAATCT	NCTNTTCTGC	TTGGTGGACA	GCACCANTNA	600
CTGTNNANCT	TTAGNCCNTG	GTCCTCNTGG	GTTGNNCTTG	AACCTAATCN	CCNNCTCAACT	660
GGGACAAGGT	AANTNGCCNT	CCTTNAATT	CCCNANCNTN	CCCCCTGGTT	TGGGGTTTTN	720
CNCNCTCCTA	CCCCAGAAAAN	NCCGTGTTCC	CCCCCAACTA	GGGGCCNAAA	CCNNTNTTC	780
CACAACCCTN	CCCCACCCAC	GGGTTCNGNT	GGTTNG			816

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAAGGCCTG	GGCAGGCATA	NACTTGAAGG	TACAACCCCA	GGAACCCCTG	GTGCTGAAGG	60
ATGTGGAAAA	CACAGATTGG	CGCCTACTGC	GGGGTGACAC	GGATGTCAGG	GTAGAGAGGA	120
AAGACCCAAA	CCAGGTGGAA	CTGTGGGGAC	TCAAGGAANG	CACCTACCTG	TTCCAGCTGA	180
CAGTGACTAG	CTCAGACCAC	CCAGAGGACA	CGGCCAACGT	CACAGTCACT	GTGCTGTCCA	240
CCAAGCAGAC	AGAAGACTAC	TGCCTCGCAT	CCAACAANGT	GGGTCGCTGC	CGGGGCTCTT	300
TCCCCACGCTG	GTACTATGAC	CCCACGGAGC	AGATCTGCAA	GAGTTTCGTT	TATGGAGGCT	360
GCTTGGGCAA	CAAGAACAAAC	TACCTTCGGG	AAGAAGAGTG	CATTCTANCC	TGTCNGGGTG	420
TGCAAGGTGG	GCCTTTGANA	NGCANCTCTG	GGGCTCANGC	GACTTTCCCC	CAGGGCCCT	480
CCATGGAAAG	GCGCCATCCA	NTGTTCTCTG	GCACCTGTCA	GCCCACCCAG	TTCCGCTGCA	540
NCAATGGCTG	CTGCATCNAC	ANTTTCTNG	AATTGTGACA	ACACCCCCCA	NTGCCCCCAA	600
CCCTCCCAAC	AAAGCTTCCC	TGTTAAAAAA	TACNCCANTT	GGCTTTNAC	AAACNCCCGG	660
CNCCTCCNTT	TTCCCCNNTN	AACAAAGGGC	NCTNGCNTTT	GAAC TGCCCN	AACCCNGGAA	720
TCTNCCNNGG	AAAAANTNCC	CCCCCTGGTT	CCTNNAANCC	CCTCCNCNA	ANCTNCCCCC	780
CCC						783

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCCCAATTG	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTTGGAT	GTCATACAAA	60
AGCTGATTGA	AGCAACCCCTC	TACTTTTGG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTTCA	120
TTGGCTGTGT	TGGTGACGTT	GTCATTGCAA	CAGAATGGGG	GAAAGGCACT	GTTCTCTTG	180
AAGTAGGGTG	AGTCCTCAAA	ATCCGTATAG	TTGGTGAAGC	CACAGCACTT	GAGCCCTTTC	240
ATGGTGGTGT	TCCACACTTG	AGTGAAGTCT	TCCTGGGAAC	CATAATCTTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCAG	GAAGTGCTCA	GCCATTGTGG	TGTACACCAA	GGCGACCACA	360
GCAGCTGCAA	CCTCAGCAAT	GAAGATGAGG	AGGAGGATGA	AGAAGAACGT	CNCGAGGGCA	420
CACTTGCTCT	CCGTCTTAGC	ACCATAGCAG	CCCANGAAAC	CAAGAGCAA	GACCACAAACG	480
CCNGCTGCGA	ATGAAAGAAA	NTACCCACGT	TGACAAACTG	CATGGCCACT	GGACGACAGT	540
TGGCCCGAAN	ATCTTCAGAA	AAGGGATGCC	CCATCGATTG	AACACCCANA	TGCCCACACTGC	600
CNAACAGGGCT	GCNCCNCNCN	GAAAGAATGA	GCCATTGAAG	AAGGATCNTC	NTGGTCTTAA	660
TGAAC TGAAA	CCNTGCATGG	TGGCCCTGT	TCAGGGCTCT	TGGCAGTGAA	TTCTGANAAA	720
AAGGAACNGC	NTNAGCCCCC	CCAAANGANA	AAACACCCCC	GGGTGTTGCC	CTGAATTGGC	780
GGCCAAGGAN	CCCTGCCCN	G				801

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGAGAGCCA	GGCGTCCCTC	TGCCTGCCCA	CTCAGTGGCA	ACACCCGGGA	GCTGTTTGT	60
CCTTGTTGGA	GCCTCAGCAG	TTCCCTCTTT	CAGAACTCAC	TGCCAAGAGC	CCTGAACAGG	120
AGCCACCATG	CAGTGCTTCA	GCTTCATTAA	GACCATGATG	ATCCTCTTCA	ATTTGCTCAT	180
CTTTCTGTGT	GGTGCAAGCCC	TGTTGGCAGT	GGGCATCTGG	GTGTCAATCG	ATGGGGCATC	240
CTTTCTGAAG	ATCTTCGGGC	CACTGTCGTC	CAGTGCATG	CAGTTGTCA	ACGTGGGCTA	300
CTTCCTCATC	GCAGCCGGCG	TTGTGGTCTT	TGCTCTTGGT	TTCCTGGGCT	GCTATGGTGC	360

TAAGACGGAG AGCAAGTGTG CCCTCGTGAC GTTCTTCTTC ATCCTCCTCC TCATCTTCAT	420
TGCTGAAGTT GCAGCTGCTG TGGTCGCCTT GGTGTACACC ACAATGGCTG AACCAATTCCCT	480
GACGTTGCTG GTANTGCCTG CCATCAANAA AGATTATGGG TTCCCAGGAA AAATTCACTC	540
AANTNTGGAA CACCNCCATG AAAAGGGCTC CAATTCTGN TGGCTTCCCC AACTATAACG	600
GAATTTGAA AGANTCNCCT TACTTCCAAA AAAAAANANT TGCCTTNCC CCCNTTCTGT	660
TGCAATGAAA ACNTCCCAAN ACNGCCAATN AAAACCTGCC CNNNAAAAAA GGNTCNAAA	720
CAAAAAAANT NNAAGGGTTN	740

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCGCTGGTTG CGCTGGTCCA GNGNAGCCAC GAAGCACGTC AGCATAACACA GCCTCAATCA	60
CAAGGTCTTC CAGCTGCCGC ACATTACGCA GGGCAAGAGC CTCCAGCAAC ACTGCATATG	120
GGATACACTT TACTTAGCA GCCAGGGTGA CAACTGAGAG GTGTCGAAGC TTATTCTTCT	180
GAGCCTCTGT TAGTGGAGGA AGATTCCGGG CTTCAAGCTAA GTAGTCAGCG TATGTCCCCT	240
AAGCAAACAC TGTGAGCAGC CGGAAGGTAG AGGCAAAGTC ACTCTCAGCC AGCTCTCTAA	300
CATTGGGCAT GTCCAGCAGT TCTCCAAACA CGTAGACACC AGNGGCCTCC AGCACCTGAT	360
GGATGAGTGT GGCCAGCGCT GCCCCCTTGG CCGACTTGGC TAGGAGCAGA AATTGCTCCT	420
GGTTCTGCCCG TGTCAACCTTC ACTTCCGCAC TCATCACTGC ACTGAGTGTG GGGGACTTGG	480
GCTCAGGATG TCCAGAGACG TGGTTCCGCC CCCTCNCTTA ATGACACCGN CCANNCAACC	540
GTCGGCTCCC GCCGANTGNG TTCGTCGTNC CTGGGTCAAGG GTCTGCTGGC CNCTACTTGC	600
AANCTTCGTC NGGCCCATGG AATTCAACCNC ACCGGAACTN GTANGATCCA CTNNNTCTAT	660
AACCAGNCGC CACCGCNNNT GGAACCTCCAC TCTTNTNCC TTTACTTGAG GGTTAAGGTC	720
ACCCTNNCG TTACCTTGGT CCAAACCTN CCNTGTGTCG ANATNGTNAA TCNGGNCCNA	780
TNCCANCCNC ATANGAAGCC NG	802

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CNAAGCTTCC AGGTNACGGG CCGCNAANCC TGACCCNAGG TANCANAANG CAGNCNGGG	60
GAGCCCACCG TCACGNNGNG GNGTCTTTAT NGGAGGGGGC GGAGCCACAT CNCTGGACNT	120
CNTGACCCCA ACTCCCCNCC NCNCANTGCA GTGATGAGTG CAGAACTGAA GGTNACGTGG	180
CAGGAACCAA GANCAAANN NC TGCTCCNNTC CAAGTCGGCN NAGGGGGCGG GGCTGGCCAC	240
GCNCATCCNT CNAGTGTGN AAAGCCCCNN CCTGTCTACT TGTTTGGAGA ACNGCENNNA	300
CATGCCCAAGN GTTANATAAC NGGCNGAGAG TNANTTGCC TCTCCCTTCC GGCTGCGCAN	360
CGNGTNTGCT TAGNGGACAT AACCTGACTA CTTAACTGAA CCCNNGAATC TNCCNCCCT	420
CCACTAAGCT CAGAACAAAA AACTTCGACA CCAACTCANTT GTCACCTGNC TGCTCAAGTA	480
AAGTGTACCC CATNCCAAT GTNTGCTNGA NGCTCTGNCC TGCNTTANGT TCGGTCTGG	540
GAAGACCTAT CAATTNAAGC TATGTTCTG ACTGCCTCTT GCTCCCTGNA ACAANCNACC	600
CNNCNNTCCA AGGGGGGGNC GGCCCCCAAT CCCCCCAACC NTNAATTNAN TTTANCCCN	660
CCCCCNNGCC CGGCCTTTA CNANCNTCNN NNACNGGNA AAACCNNGC TTTNCCCAAC	720
NNAATCCNCC T	731

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTTTTTTTT	TTTTTTTTTT	TAAAAACCCC	CTCCATTNAA	TGNAAACTTC	CGAAATTGTC	60
CAACCCCTC	NTCCAAATNN	CCNTTCCGG	GNGGGGTTC	CAAACCCAAN	TTANNTTGG	120
ANNTTAAATT	AAATNTTNNT	TGGNGGNNA	ANCCNAATGT	NANGAAAGTT	NAACCCANTA	180
TNANCTTNA	TNCCTGGAAA	CCNGTNGNTT	CCAAAAATNT	TTAACCCCTTA	ANTCCCTCCG	240
AAATNGTTNA	NGGAAAACCC	AANTTCTCNT	AAGGTTGTTT	GAAGGNTNAA	TNAAAANCCC	300
NNCCAATTGT	TTTNGGCCAC	GCCTGAATTA	ATTGGNTTCC	GNTGTTTCC	NTTAAAANAA	360
GGNNANCCCC	GGTTANTNAA	TCCCCCCNNC	CCCAATTATA	CCGANTTTT	TTNGAATTGG	420
GANCCNCGG	GAATTAACGG	GGNNNNNTCCC	TNTTGGGGGG	CNGGNCCCC	CCCCNTCGGG	480
GGTTNGGGNC	AGGNCCNAAT	TGTTTAAGGG	TCCGAAAAAT	CCCTCCNAGA	AAAAAAANCTC	540
CCAGGNTGAG	NNTNGGGTTT	NCCCCCCCCC	CANGGCCCCT	CTCGNANAGT	TGGGGTTTGG	600
GGGGCCTGGG	ATTNTNTTTC	CCCTNTTNCC	TCCCCCCCCC	CCNGGGANAG	AGGTTNGNGT	660
TTTGNTCNNC	GGCCCCNCCN	AAGANTTTN	CCGANTTNAN	TTAAATCCNT	GCCTNGGCGA	720
AGTCCNTTGN	AGGGNTAAAN	GGCCCCCTNN	CGGG			754

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATCANCCCAT	GACCCNAAC	NNGGGACCN	TCANCCGGNC	NNNCNACCNC	CGGCCNATCA	60
NNGTNAGNNC	ACTNCNNNTN	NATCACNCCC	CNCCNACTAC	GCCCNCNANC	CNACGNCTA	120
NNCANATNCC	ACTGANNGCG	CGANGTNGAN	NGAGAAANCT	NATACCANAG	NCACCANACN	180
CCAGCTGTCC	NANAANGCCT	NNNATAACNGG	NNNATCCAAT	NTGNANCCTC	CNAAGTATTN	240
NNCNCCNAT	GATTTCCCTN	ANCCGATTAC	CCNTNCCCC	TANCCCTCC	CCCCAACNA	300
CGAAGGCNCT	GGNCCNAAGG	NNCGCNCC	CCGCTAGNTC	CCCNCAAGT	CNCNCNCTA	360
AACTCANCCN	NATTACNCGC	TTCNTGAGTA	TCACTCCCC	AATCTCACCC	TACTCAACTC	420
AAAAANATCN	GATACAAAAT	AATNCAAGCC	TGNTTATNAC	ACTNTGACTG	GGTCTCTATT	480
TTAGNGGTCC	NTNAANCNTC	CTAATACTTC	CAGTCTNCCT	TCNCCAATT	CCNAANGGCT	540
CTTTCNGACA	GCATNTTTG	GTTCCNNNT	GGGTTCTTAN	NGAATTGCC	TTCNTNGAAC	600
GGGCTCNTCT	TTTCCTTCGG	TTANCTGGN	TTCNNCCGGC	CAGTTATTAT	TTCCCNNTT	660
AAATCNTNC	CNTTANTTT	TGGCNTTCNA	AACCCCCGGC	CTTGAAAACG	GCCCCCTGGT	720
AAAAGGTTGT	TTTGANAAAA	TTTTGTTTT	GTTCC			755

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTTTTTTT	TTTTTANGTG	TNGTCGTGCA	GGTAGAGGCT	TACTACAANT	GTGAANACGT	60
ACGCTNGGAN	TAANGCGACC	CGANTTCTAG	GANNCNCCT	AAAATCANAC	TGTGAAGATN	120
ATCCTGNNA	CGGAANGGTC	ACCGGNNNGAT	NNTGCTAGGG	TGNCCNCTCC	CANNNCNTTN	180
CATAACTCNG	NGGCCCTGCC	CACCACCTTC	GGCGGCCNG	NGNCCGGGCC	CGGGTCATTN	240
GNNTTAACCN	CACTNNGCNA	NCGGTTCCN	NCCCCNNNG	ACCCNGGCAG	TCCGGGGTNC	300
TCTGTCTTCC	CCTGNAGNCN	ANAAANTGGG	CCNCGGNCCC	CTTTACCCCT	NNACAAGCCA	360
CNGCCNTCTA	NCCNCNGCCC	CCCCTCCANT	NNGGGGACT	GCCNANNCT	CCGTTNCTNG	420
NNACCCNNN	GGGTNCCTCG	GTTGTCGANT	CNACCGNANG	CCANGGATT	CNAAGGAAGG	480
TGCGTTNTTG	GCCCCTACCC	TTCGCTNCGG	NNCACCCCTC	CCGACNANGA	NCCGCTCCCG	540
CNCNCGNNG	CCTCNCCCTG	CAACACCCGC	NCTCNTCNGT	NCGGNNNCCC	CCCCACCCGC	600
NCCCTNCNC	NGNCGNANCN	CTCCNCCNCC	GTCTCANNCA	CCACCCCGCC	CGGCCAGGCC	660
NTCANCCACN	GGNNGACNNG	NAGCNCNNTC	GCNCCGCGCN	GCGNCNCCT	CGCCNCNGAA	720
CTNCNTCNGG	CCANTNNCGC	TCAANCCNA	CNAAACGCCG	CTGCGCGGCC	CGNAGCGNCC	780
NCCTCCNCGA	GTCCTCCGN	CTTCCNACCC	ANGNNTTCCN	CGAGGACACN	NNACCCGCC	840
	NNCANGCGG					849

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCGCAAACTA	TACTTCGCTC	GNACTCGTGC	GCCTCGCTNC	TCTTTCTC	CGCAACCATG	60
TCTGACNANC	CCGATTNGGC	NGATATCNAN	AAGNTCGANC	AGTCCAACT	GANTAACACA	120
CACACNCNAN	AGANAAATCC	NCTGCCTTCC	ANAGTANACN	ATTGAACNNG	AGAACCAANGC	180
NGGCGAATCG	TAATNAGGCG	TGCGCCGCCA	ATNTGTCNCC	GTTTATTNTN	CCAGCNTCNC	240
CTNCCNACCC	TACNTCTCN	NAGCTGTCNN	ACCCCTNGTN	CGNACCCCCC	NAGGTCGGGA	300
TCGGGTTTNN	NNTGACCGNG	CNNCCCTCC	CCCCNTCCAT	NACGANCCNC	CCGCACCACC	360
NANNGCNCG	NCCCCNNCT	CTTCGCCNCC	CTGTCCTNTN	CCCCTGTNGC	CTGGCNCNGN	420
ACCGCATTGA	CCCTCGCCNN	CTNCNNGAAA	NCGNANACGT	CCGGGTTGNN	ANNANCGCTG	480
TGGGNNNNGCG	TCTGCNCCGC	GTTCCCTTCCN	NCNNCTTCCA	CCATCTTCNT	TACNGGGTCT	540
CCNCGCCNTC	TCNNNCACNC	CCTGGGACGC	TNTCCTNTGC	CCCCCTTNAC	TCCCCCCCCTT	600
CGNCGTGNCC	CGNCCCCACC	NTCATTNCA	NACGNTCTTC	ACAANNNCCT	GGNTNNCTCC	660
CNANCNGNCN	GTCANCCNAG	GGAAGGGNGG	GGNNCCNNTG	NTTGACGTTG	NGGNGANGTC	720
CGAANANTCC	TCNCCNTCAN	CNCTACCCCT	CGGGCGNNCT	CTCNGTTNCC	AACTTANCAA	780
NTCTCCCCCG	NGNGCNCNTC	TCAGCCTCNC	CCNCCCCNCT	CTCTGCANTG	TNCTCTGCTC	840
TNACCNNTAC	GANTNTTCGN	CNCCCTCTT	CC			872

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCATGCAAGC	TTGAGTATT	TATAGNGTCA	CCTAAATANC	TTGGCNTAAT	CATGGTCNTA	60
NCTGNCTTCC	TGTGTCAAAT	GTATACNAAN	TANATATGAA	TCTNATNTGA	CAAGANNGTA	120

TCNTNCATTA	GTAACAANTG	TNNTGTCCAT	CCTGTCNGAN	CANATTCCA	TNNATTNCGN	180
CGCATTNCN	GCNCANTATN	TAATNGGGAA	NTCNNTNNN	NCACCNNCAT	CTATCNTNCC	240
GCNCCTGAC	TGGNAGAGAT	GGATNANTTC	TNNTNTGACC	NACATGTTCA	TCTTGGATTN	300
AANANCCCCC	CGCNGNCCAC	CGGTTNGNNG	CNAGCCNNTC	CCAAGACCTC	CTGTGGAGGT	360
AACCTGCGTC	AGANNCATCA	AACNTGGAA	ACCCGCNNCC	ANGTNNAAGT	NGNNNCANAN	420
GATCCCGTCC	AGGNTTNACC	ATCCCTTCNC	AGCGCCCCCT	TTNGTGCCTT	ANAGNGNAGC	480
GTGTCCNANC	CNCTCAACAT	GANACGCGCC	AGNCCANCCG	CAATTNGGCA	CAATGTCGNC	540
GAACCCCCTA	GGGGGANTNA	TNCAAANCCC	CAGGATTGTC	CNCNCANGAA	ATCCCNCANC	600
CCCNCCCTAC	CCNNCTTGG	GACNGTGACC	AANTCCCGGA	GTNCCAGTCC	GGCCNGNCTC	660
CCCCACCGGT	NNCCNTGGGG	GGGTGAANCT	CNGNNTCANC	CNGNCAGGNN	NTCGNAAGGA	720
ACCGGNCTN	GGNCGAANNG	ANCNNTCNGA	AGNGCCNCNT	CGTATAACCC	CCCCTCNCCA	780
NCCNACNGNT	AGNTCCCCCC	CNGGGTNCGG	AANGG			815

## (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 775 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGAGATGTC	TCGCTCCGTG	GCCTTAGCTG	TGCTCGCGCT	ACTCTCTCTT	TCTGGCCTGG	60
AGGCTATCCA	GCGTACTCCA	AAGATTCAAGG	TTTACTCAGC	TCATCCAGCA	GAGAATGGAA	120
AGTCAAATT	CCTGAATTGC	TATGTGTCTG	GGTTTCATCC	ATCCGACATT	GAANTTGACT	180
TACTGAAGAA	TGGANAGAGA	ATTGAAAAAG	TGGAGCATTC	AGACTTGTCT	TTCAGCAAGG	240
ACTGGTCTT	CTATCTCNTG	TACTACACTG	AATTCACCCCC	CACTGAAAAAA	GATGAGTATG	300
CCTGCCGTGT	GAACCATGTG	ACTTTGTAC	AGCCCAAGAT	AGTTAAGTGG	GATCGAGACA	360
TGTAAGCAGN	CNNCATGGAA	GTTTGAAGAT	GCCGCATTTG	GATTGGATGA	ATTCCAAATT	420
CTGCTTGCTT	GCNTTTAAT	ANTGATATGC	NTATACACCC	TACCCTTTAT	GNCCCCAAAT	480
TGTAGGGTT	ACATNANTGT	TCNCNTNGGA	CATGATCTTC	CTTTATAANT	CCNCCNTTCG	540
AATTGCCGT	CNCCNGTTN	NGAATGTTTC	CNNAACCACG	GTTGGCTCCC	CCAGGTCNCC	600
TCTTACGGAA	GGGCCTGGGC	CNCTTNCAA	GGTTGGGGGA	ACCNAAAATT	TCNCTNTGC	660
CCNCCCNCCA	CNNTCTTNG	NNCNCANTTT	GGAACCTTC	CNATTCCCC	TGGCCTCNNA	720
NCCTTNNCTA	ANAAAACTTN	AAANCGTNGC	NAAANNTTN	ACTTCCCCCC	TTACC	775

## (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 820 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ANATTANTAC	AGTGTAAATCT	TTTCCCAGAG	GTGTGTANAG	GGAACGGGGC	CTAGAGGCAT	60
CCCANAGATA	NCTTATANCA	ACAGTGCTTT	GACCAAGAGC	TGCTGGGCAC	ATTTCCTGCA	120
GAAAAGGTGG	CGGTCCCCAT	CACTCCTCCT	CTCCCATAGC	CATCCCAGAG	GGGTGAGTAG	180
CCATCANGCC	TTCGGTGGGA	GGGAGTCANG	GAAACAACAN	ACCACAGAGC	ANACAGACCA	240
NTGATGACCA	TGGGCGGGAG	CGAGCCTCTT	CCCTGNACCG	GGGTGGCANA	NGANAGCCTA	300
NCTGAGGGGT	CACACTATAA	ACGTTAACGA	CCNAGATNAN	CACCTGCTTC	AAGTGCACCC	360
TTCCTACCTG	ACNACCAGNG	ACCNNAACT	GCNGCCTGGG	GACAGCNCTG	GGANCAGCTA	420
ACNNAGCACT	CACCTGCC	CCCATGGCCG	TNCGCNTCCC	TGGCCTGNC	AAGGGAAGCT	480
CCCTGTTGGA	ATTNCGGGG	NACCAAGGGA	NCCCCCTCCT	CCANCTGTGA	AGGAAAANN	540
GATGGAATT	TNCCCTTCCG	GCCNNTCCCC	TCTTCCTTTA	CACGCCCCCT	NNTACTCN	600

TCCCTCT...	T	NTCCTGNCNC	ACTTTNACC	CCNNNATTG	CCTTNATTGA	TCGGANNCTN	660
GANATTCCAC	TNNCGCCTNC	CNTCNATCNG	NAANACNAAA	NACTNTCTNA	CCCNGGGAT	720	
GGGNNCCTCG	NTCATCCTCT	CTTTTCNCT	ACCNCNNNT	CTTGCCCTCT	CCTTNGATCA	780	
TCCAACCNTC	GNTGCCNTN	CCCCCCCCNN	TCCTTNCCCC			820	

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCTGGGTGAT	GGCCTCTTCC	TCCTCAGGGA	CCTCTGACTG	CTCTGGGCCA	AAGAATCTCT	60
TGTTTCTTCT	CCGAGCCCCA	GGCAGCGGTG	ATTCAGCCCT	GCCCAACCTG	ATTCTGATGA	120
CTGCGGATGC	TGTGACGGAC	CCAAGGGCA	AATAGGGTCC	CAGGGTCCAG	GGAGGGGCGC	180
CTGCTGAGCA	CTTCCGCCCC	TCACCCCTGCC	CAGCCCCTGC	CATGAGCTCT	GGGCTGGGTC	240
TCCGCCTCCA	GGGTTCTGCT	CTTCCANGCA	NGCCANCAAG	TGGCGCTGGG	CCACACTGGC	300
TTCTTCCCTGC	CCCNCTCCCTG	GCTCTGANTC	TCTGTCTTCC	TGTCCTGTGC	ANGNCNCCTTG	360
GATCTCAGTT	TCCCTCNCTC	ANNGAACTCT	GTTTCTGANN	TCTTCANTTA	ACTNTGANTT	420
TATNACCNAN	TGGNCTGTNC	TGTCNNACTT	TAATGGGCCN	GACCGGCTAA	TCCCTCCCTC	480
NCTCCCTTCC	ANTTCNNNNNA	ACCNGCTNC	CNTCNTCTCC	CCNTANCCG	CCNGGGAANC	540
CTCCTTTGCC	CTNACCANGG	GCCNNNACCG	CCCNTNNCTN	GGGGGGCNNG	GTNNCTNCNC	600
CTGNTNNCCC	CNCTCNCNNT	TNCCTCGTCC	CNNCNCNCGN	NNGCANNTTC	NCNGTCCNN	660
TNNCTCTTCN	NGTNTCGNAA	NGNTNCNTN	TNNNNNGNCN	NGNTNNTNCN	TCCCTCTCNC	720
CNNNTGNANG	TNNTTNNNNC	NCNGNNCCCC	NNNNCNNNNN	NGGNNNTNNN	TCTNCNCNGC	780
CCCNCCCCC	NGNATTAAGG	CCTCCNNTCT	CCGGCCNC			818

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGAAGGGCG	GAGGGATATT	GTANGGGATT	GAGGGATAGG	AGNATAANGG	GGGAGGTGTG	60
TCCCAACATG	ANGGTGNNGT	TCTCTTTGA	ANGAGGGTTG	NGTTTTANN	CCNGGTGGGT	120
GATTNAACCC	CATTGTATGG	AGNAAAGGN	TTTNAGGGAT	TTTCGGCTC	TTATCAGTAT	180
NTANATTCCCT	GTNAATCGGA	AAATNATNTT	TCNNCNGAA	AATNTTGCTC	CCATCCGNAA	240
ATTNCTCCCG	GGTAGTGCAT	NTTNGGGGN	CNGCCANGTT	TCCCAGGCTG	CTANAATCGT	300
ACTAAAGNTT	NAAGTGGAN	TNCAAATGAA	AACCTNNCAC	AGAGNATCCN	TACCCGACTG	360
TNNNTTNCCCT	TCGCCCTNTG	ACTCTGCNN	AGCCAATAC	CCNNNGNAT	GTCNCCCGN	420
NNNGCGNCNC	TGAAANNNNC	TCGNGGCTNN	GANCATCANG	GGGTTTCGCA	TCAAAAGCNN	480
CGTTTCNCAT	NAAGGCACTT	TNGCCTCATC	CAACCNCTNG	CCCTCNCNNCA	TTTNGCCGTC	540
NGGTTCNCCCT	ACGCTNNTNG	CNCCTNNNTN	GANATTTCNC	CCGCCTNGGG	NAANCCTCCT	600
GNAATGGGT	GGGNCTTNTC	TTTTNACCNN	GNGGTNTACT	AATCNCTNC	ACGCNTNCTT	660
TCTCNACCCCC	CCCCCTTTTT	CAATCCCANC	GGCNAATGGG	GTCTCCCN	CGANGGGGG	720
NNNCCCANNC	C					731

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGGNCNC	TTCTATGANT	ANTNTTAGAT	60
CGCTCANACC	TCACANCCCTC	CCNACNANGC	CTATAANGAA	NANNAATAGA	NCTGTNCNN	120
ATNTNTACNC	TCATANNCTC	CNNNACCCAC	TCCCTCTTAA	CCCNTACTGT	GCCTATNGCN	180
TNNCTANTCT	NTGCCGCCTN	CNANCCACCN	GTGGGCCNAC	CNCNNGNATT	CTCNATCTCC	240
TCNCCATNTN	GCCTANANTA	NGTNCATACC	CTATACCTAC	NCCAATGCTA	NNNCTAANCN	300
TCCATNANTT	ANNNTAACTA	CCACTGACNT	NGACTTTNC	ATNANCTCCT	AATTGAAATC	360
TACTCTGACT	CCCACNGCCT	ANNNATTAGC	ANCNTCCCCC	NACNATNTCT	CAACCAAATC	420
NTCAACAACC	TATCTANCTG	TTCNCCAACC	NTTNCCCTCG	ATCCCCNNAC	AACCCCCCTC	480
CCAAATACCC	NCCACCTGAC	NCCTAACCCN	CACCATCCCC	GCAAGCCNAN	GGNCATTTAN	540
CCACTGGAAT	CACNATNGGA	NAAAAAAAAC	CCNAACTCTC	TANCNCNNAT	CTCCCTAANA	600
AATNCTCCTN	NAATTTACTN	NCANTNCCAT	CAANCCCACN	TGAAACNNAA	CCCCCTGTTT	660
TANATCCCTT	CTTTCGAAAAA	CCNACCCTT	ANNNCCCAAC	CTTNNGGCC	CCCCCTNC	720
CCNAATGAAG	GNCNCCAAT	CNANGAAACG	NCCNTGAAAA	ANCNAGGCNA	ANANNNTCCG	780
CANATCCTAT	CCCTTANTTN	GGGGNCCCTT	NCCCNGGCC	CC		822

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGGCCGCCTG	CTCTGGCACA	TGCCTCCTGA	ATGGCATCAA	AAGTGATGGA	CTGCCATTG	60
CTAGAGAAGA	CCTTCTCTCC	TACTGTCATT	ATGGAGCCCT	GCAGACTGAG	GGCTCCCCTT	120
GTCTGCAGGA	TTTGATGTCT	GAAGTCGTGG	AGTGTGGCTT	GGAGCTCCTC	ATCTACATNA	180
GCTGGAAGCC	CTGGAGGGCC	TCTCTCGCCA	GCCTCCCCCT	TCTCTCCACG	CTCTCCANGG	240
ACACCAGGGG	CTCCAGGCAG	CCCATTATTC	CCAGNANGAC	ATGGTGTTC	TCCACGCGGA	300
CCCATGGGGC	CTGNAAGGCC	AGGGTCTCCT	TTGACACCAT	CTCTCCGTC	CTGCCTGGCA	360
GGCCGTGGGA	TCCACTANTT	CTANAACGGN	CGCCACCNCG	GTGGGAGCTC	CAGTTTTGT	420
TCCCTTTAAT	GAAGGTTAAT	TGCNCGCTTG	GCGTAATCAT	NGGTCANAAC	TNTTCCTGT	480
GTGAAATTGT	TTNTCCCCTC	NCNATTCCNC	NCNACATACN	AACCCGGAAN	CATAAAAGTGT	540
TAAAGCCTGG	GGGTNGCCTN	NNGAATNAAC	TNAACTCAAT	TAATTGCGTT	GGCTCATGGC	600
CCGCTTTCCN	TTCNGGAAAA	CTGTCNTCCC	CTGCNTTNN	GAATCGGCCA	CCCCCCNGGG	660
AAAAGCGGTT	TGCNTTTNG	GGGGNTCCTT	CCNCTTCCCC	CCTCNCTAAN	CCCTNCGCCT	720
CGGTCGTTNC	NGGTNGCGGG	GAANGGGNAT	NNNCTCCNC	NAAGGGGNG	AGNNNGNTAT	780
CCCCAAA						787

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTTTTTTT	TTTTTTGGC	GATGCTACTG	TTAATTGCA	GGAGGTGGGG	GTGTGTGTAC	60
CATGTACCA	GGCTATTAGA	AGCAAGAAGG	AAGGAGGGAG	GGCAGAGCGC	CCTGCTGAGC	120
AACAAAGGAC	TCCTGCAGCC	TTCTCTGTCT	GTCTCTTGGC	GCAGGCACAT	GGGGAGGCCT	180
CCCGCAGGGT	GGGGGCCACC	AGTCCAGGGG	TGGGAGCACT	ACANGGGTG	GGAGTGGGTG	240
GTGGCTGGTN	CNAATGGCCT	GNCACANATC	CCTACGATT	TTGACACCTG	GATTCACCA	300
GGGGACCTTC	TGTTCTCCCA	NGGNAACTTC	NTNNATCTCN	AAAGAACACA	ACTGTTCTT	360
CNGCANTTCT	GGCTGTTCAT	GGAAAGCACA	GGTGTCCNAT	TTNGGCTGGG	ACTTGGTACA	420
TATGGTTCCG	GCCCACCTCT	CCCNTCNAAN	AAGTAATTCA	CCCCCCCCCN	CCNTCTNTG	480
CCTGGGCCCT	TAANTACCCA	CACCGGAAC	CANTTANTTA	TTCATCTTNG	GNTGGGCTTG	540
NTNATCNCCN	CCTGAANGCG	CCAAGTTGAA	AGGCCACGCC	GTNCCCNCTC	CCCATAGNAN	600
NTTTTNNCNT	CANCTAATGC	CCCCCNNGG	AACNATCCAA	TCCCCCCCCN	TGGGGGCCCC	660
AGCCCANGGC	CCCCGNCTCG	GGNNNCCNGN	CNCGNANTCC	CCAGGNTCTC	CCANTCNGNC	720
CCNNNGCNCC	CCCGCACGCA	GAACANAAGG	NTNGAGCCNC	CGCANNNNNN	NGGTNNCNAC	780
CTCGCCCCCCC	CCNNCGNNG					799

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	60
TTTTNCCNAG	GGCAGGTTA	TTGACAACCT	CNCGGACAC	AANCAGGCTG	GGGACAGGAC	120
GGCAACAGGC	TCCGGCGCG	GGCGCGCGG	CCCTACCTGC	GGTACCAAAT	NTGCAGCCTC	180
CGCTCCCGCT	TGATNTTCCT	CTGCAGCTGC	AGGATGCCNT	AAAACAGGGC	CTCGGCCNTN	240
GGTGGGCACC	CTGGGATTN	AATTTCCACG	GGCACAAATGC	GGTCGCANCC	CCTCACCAACC	300
NATTAGGAAT	AGTGGTNTA	CCCNCCNCCG	TTGGCNCACT	CCCCNTGGAA	ACCACTTNTC	360
GCGGCTCCGG	CATCTGGTCT	TAAACCTTGC	AAACNCTGGG	GCCCTCTTT	TGGTTANTNT	420
NCCNGCCACA	ATCATNACTC	AGACTGGCNC	GGGCTGGCCC	AAAAAAANCN	CCCCAAAACC	480
GNCCATGTC	TTNNCGGGGT	TGCTGCNATN	TNCATCACCT	CCCGGGCNCA	NCAGGNCAAC	540
CCAAAAGTTC	TTGNGGCCCN	CAAAAAANCT	CCGGGGGGNC	CCAGTTCAA	CAAAGTCATC	600
CCCCTTGGCC	CCCAAATCCT	CCCCCCGNTT	NCTGGTTTG	GGAACCCACG	CCTCTNNCTT	660
TGGNNGGCAA	GNTGGNTCCC	CCTTCGGGCC	CCCGGTGGGC	CCNNCTCTAA	NGAAAACNCC	720
NTCCTNNNCA	CCATCCCCC	NNGNNAACGNC	TANCAANGNA	TCCCTTTTT	TANAAACGGG	780
CCCCCCNCG						789

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACAGAACAT	GTTGGATGGT	GGAGCACCTT	TCTATACGAC	TTACAGGACA	GCAGATGGGG	60
AATTCAATGGC	TGTTGGAGCA	ATANAACCCC	AGTTCTACGA	GCTGCTGATC	AAAGGACTTG	120
GACTAAAGTC	TGATGAACTT	CCCAATCAGA	TGAGCATGGA	TGATTGCCA	GAAATGAANA	180
AGAAGTTTGC	AGATGTATTT	GCAAAGAAGA	CGAAGGCAGA	GTGGTGTCAA	ATCTTTGACG	240
GCACAGATGC	CTGTGTGACT	CCGGTTCTGA	CTTTTGAGGA	GGTTGTTCAT	CATGATCACA	300

ACAANGAACG	GGGCTCGTT	ATCACCANTG	AGGAGCAGGA	CGTGAGCCCC	CGCCCTGCAC	360
CTCTGCTGTT	AAACACCCCA	GCCATCCCTT	CTTCAAAAG	GGATCCACTA	CTTCTAGAGC	420
GGNCGCCACC	GCGGTGGAGC	TCCAGCTTT	GTTCCCTTA	GTGAGGGTTA	ATTGCGCGCT	480
TGGCGTAATC	ATGGTCATAN	CTGTTCTG	TGTGAAATTG	TTATCCGCTC	ACAATTCCAC	540
ACAACATACG	ANCCGGAAGC	ATNAAATTT	AAAGCCTGGN	GGTNGCCTAA	TGANTGAACT	600
NACTCACATT	AATTGGCTTT	GCGCTCACTG	CCCGCTTCC	AGTCCGGAAA	ACCTGTCTT	660
GCCAGCTGCC	NTTAATGAAT	CNGGCCACCC	CCCGGGAAA	AGGCNGTTG	CTTNTTGGGG	720
CGCNCTTCCC	GCTTCTCGC	TTCCTGAANT	CCTTCCCCCC	GGTCTTCGG	CTTGCGGCNA	780
ACGGTATCNA	CCT					793

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCCGCACCG	GCATGTACGA	GCAACTCAAG	GGCGAGTGG	ACCGTAAAAG	CCCCAATCTT	60
ANCAAGTGC	GGGAANAGCT	GGGTCGACTC	AAGCTAGTTC	TTCTGGAGCT	CAACTTCTTG	120
CCAACCACAG	GGACCAAGCT	GACCAACAG	CAGCTAATT	TGGCCCGTGA	CATACTGGAG	180
ATCGGGGCC	AATGGAGCAT	CCTACGCAAN	GACATCCCCT	CCTTCGAGCG	CTACATGGCC	240
CAGCTCAAAT	GCTACTACTT	TGATTACAAN	GAGCAGCTCC	CCGAGTCAGC	CTATATGCAC	300
CAGCTCTTGG	GCCTCAACCT	CCTCTTCTG	CTGTCCCAGA	ACCGGGTGGC	TGANTNCCAC	360
ACGGANTTGG	ANCGGCTGCC	TGCCCAANGA	CATACANACC	AATGTCTACA	TCNACCACCA	420
GTGTCCCTGGA	GCAAACTGA	TGGANGGCAG	CTACCNAAA	GTNTTCTGG	CCNAGGGTAA	480
CATCCCCCGC	CGAGAGCTAC	ACCTTCTTCA	TTGACATCCT	GCTCGACACT	ATCAGGGATG	540
AAAATCGCNG	GGTTGCTCCA	GAAAGGCTNC	AANAANATCC	TTTCNCTGA	AGGCCCGGG	600
ATNCNCTAGT	NCTAGAATCG	GCCCCGCATC	GCGGTGGANC	CTCCAACCTT	TCGTTNCCCT	660
TTACTGAGGG	TTNATTGCCG	CCCTTGGCGT	TATCATGGTC	ACNCCNGTT	CCTGTGTTGA	720
AATTNTTAAC	CCCCCACAA	TCCACGCCNA	CATTNG			756

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGGATCTCT	ANATCNACCT	GNATGCATGG	TTGTCGGTGT	GGTCGCTGTC	GATGAANATG	60
AACAGGATCT	TGCCCTTGAA	GCTCTCGGCT	GCTGTNTTA	AGTTGCTCAG	TCTGCCGTCA	120
TAGTCAGACA	CNCTCTTGGG	CAAAAAACAN	CAGGATNTGA	GTCTTGATT	CACCTCCAAT	180
AATCTCNGG	GCTGTCTGCT	CGGTGAAC	GATGACNANG	GGCAGCTGGT	TGTGTNTGAT	240
AAANTCCANC	ANGTTCTCCT	TGGTGACCTC	CCCTTCAAAG	TTGTTCCGGC	CTTCATCAA	300
CTTCTNNAAAN	ANGANNANCC	CANCTTGTC	GAGCTGGNAT	TTGGANAACA	CGTCACTGTT	360
GGAAACTGAT	CCCAAATGGT	ATGTCATCCA	TCGCCTCTGC	TGCCTGAAA	AAACTTGCTT	420
GGCNCAAATC	CGACTCCCCN	TCCTTGAAAG	AAGCCNATCA	CACCCCCCTC	CCTGGACTCC	480
NNCAANGACT	CTNCCGCTNC	CCCNCCNNG	CAGGGTTGGT	GGCANNCGG	GCCCNCGCG	540
TTCTTCAGCC	AGTTCACNAT	NTTCATCAGC	CCCTCTGCCA	GCTGTTNTAT	TCCTTGGGG	600
GGAANCCGTC	TCTCCCTTCC	TGAANNAACT	TTGACCGTNG	GAATAGCCGC	GCNTCNCCNT	660
ACNTNCTGGG	CCGGGTTCAA	ANTCCCTCCN	TTGNCNNCN	CCTCGGGCCA	TTCTGGATT	720
NCCNAACTTT	TTCCTTCCCC	CNCCCCNCGG	NGTTTGGNTT	TTTCATNGGG	CCCCAACTCT	780

GCTNTTGGCC ANTCCCCTGG GGGCNTNTAN CNCCCCCTNT GGTCCCNNTNG GGCC

834

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGNCGCTT	CCNGCCGCGC	CCC GTTCCA	TGACNAAGGC	TCC CTTCANG	TTAAATACNN	60
CCTAGNAAAC	ATTAATGGGT	TGCTCTACTA	ATACATCATA	CNAACCAGTA	AGCCTGCCA	120
NAACGCCAAC	TCAGGCCATT	CCTACCAAAG	GAAGAAAGGC	TGGTCTCTCC	ACCCCTGTA	180
GGAAAGGCCT	GCCTTGTAAG	ACACCACAAT	NCGGCTGAAT	CTNAAGTCTT	GTGTTTTACT	240
AATGGAAAAA	AAAAATAAAC	AANAGGTTT	GTTCTCATGG	CTGCCAACCG	CAGCCTGGCA	300
CTAAAACANC	CCAGCGCTCA	CTTCTGCTT	GANAAATATT	CTTGCTCTT	TTGGACATCA	360
GGCTTGATGG	TATCACTGCC	ACNTTCCAC	CCAGCTGGC	NCCCTTCCCC	CATNTTTGTC	420
ANTGANCTGG	AAGGCCTGAA	NCTTAGTCTC	CAAAAGTCTC	NGCCCACAAG	ACCGGCCACC	480
AGGGGANGTC	NTTTNCAGTG	GATCTGCCA	ANANTACCN	TATCATCNNT	GAATAAAAAG	540
GCCCCTGAAC	GANATGCTTC	CANCANCC	TAAGACCCAT	AATCCTNGAA	CCATGGTGCC	600
CTTCCGGTCT	GATCCNAAAG	GAATGTTCT	GGGTCCCANT	CCCTCCTTTG	TTNCTTACGT	660
TGTNTTGGAC	CCNTGCTNGN	ATNACCCAAN	TGANATCCCC	NGAAGCACCC	TNCCCCCTGGC	720
ATTGANTTT	CNTAAATTCT	CTGCCCTACN	NCTGAAAGCA	CNATTCCCTN	GGCNCCNAAN	780
GGNGAACTCA	AGAAGGTCTN	NGAAAAACCA	CNCN			814

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCATGCTGCT	CTTCCTCAAA	GTTGTTCTTG	TTGCCATAAC	AACCACCATA	GGTAAAGCGG	60	
GCGCAGTGTT	CGCTGAAGGG	GTTGTAGTAC	CAGCGCGGA	TGCTCTCCTT	GCAGAGTCCT	120	
GTGTCTGGCA	GGTCCACGCA	ATGCCCTTG	TCACTGGGA	AATGGATGCG	CTGGAGCTCG	180	
TCNAANCCAC	TCGTGTATTT	TTCACANGCA	GCCTCCTCCG	AAGCNTCCGG	GCAGTTGGGG	240	
GTGTCGTAC	ACTCCACTAA	ACTGTGATN	CANCAGCCA	TTGCTGCAGC	GGAACCTGGGT	300	
GGGCTGACAG	GTGCCAGAAC	ACACTGGATN	GGCCTTCCA	TGGAAGGCC	TGGGGAAAT	360	
CNCCTNANCC	CAAAC TGCT	CTCAAAGGCC	ACCTTGACACA	CCCCGACAGG	CTAGAAATGC	420	
ACTCTTCTTC	CCAAAGGTAG	TTGTTCTTGT	TGCCCAAGCA	NCCTCCANCA	AACCAAAANC	480	
TTGCAAAATC	TGCTCCGTGG	GGGTCA	TACCA	GGTGG	GGGAAANAA	540	
GANCCNCCTT	GT	TTGAATGC	NAAGGNAATA	ATCCTCCTGT	CTTGCTTGGG	TGGAANAGCA	600
CAATTGAACT	GT	TAACNTTG	GGCGNGTTC	CNCTNGGTG	GTCTGAAACT	AATCACCGTC	660
ACTGGAAAAAA	GGT	ANGTGCC	TTCCTTGAAT	TCCCAAANTT	CCCCTNGNTT	TGGGTNNNTT	720
CTCCTCTNCC	CTAAAATCG	TNTTCCCCCC	CCNTANGGCG			760	

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTTTTTTTT TTTTTTTTTT TTTTTAAAAA CCCCCCTCCAT TGAATGAAAA	60
CTTCCNAAAT TGTCCAACCC CCTCNCCAA ATNNCCATT CCGGGGGGGG GTTCAAACCC	120
CAAATTAATT TTGGANTTTA AATTAAATNT TNATTNGGGG AANAANCCAA ATGTNAAGAA	180
AATTTAACCC ATTATNAACT TAAATNCCTN GAAACCCNTG GNTTCCAAA ATTNTTAACC	240
CTTAAATCCC TCCGAAATTG NTAANGAAA ACCAAATTCTN CCTAAGGCTN TTTGAAGGTT	300
NGATTAAAC CCCCTTNANT TNTTTNACC CNNGNCTNAA NTATTNGNT TCCGGTGT	360
TCCTNTTAAN CNTNGGTAAC TCCCGNTAAT GAANNNCCT AANCCAATTA AACCGAATT	420
TTTTGAATT GGAAATTCCN NGGAATTNA CCGGGGTTTT TCCCNTTGG GGGCCATNCC	480
CCCNCTTCG GGGTTGGGN NTAGGTTGAA TTTTNANG NCCCAAAAAA NCCCCAANA	540
AAAAAACTCC CAAGNNTAA TTNGAATNTC CCCCTTCCCA GGCCTTTGG GAAAGGNGGG	600
TTTNTGGGGG CCNGGGANTT CNTTCCCCN TNCCNCCCC CCCCCCNNGGT AAANGTTAT	660
NGNNTTGTT TTTGGGCC CTTNANGGAC CTTCCGGATN GAAATTAAAT CCCCGGGNCG	720
GCCG	724

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TTTTTTTTTT TTTTCTTTG CTCACATTAA ATTNTTATTT TGATTTTTT TAATGCTGCA	60
CAACACAATA TTTATTCAT TTGTTCTTT TATTCATTT TATTTGTTTG CTGCTGCTGT	120
TTTATTATT TTTACTGAAA GTGAGAGGGA ACTTTGTGG CCTTTTTTCC TTTTTCTGTA	180
GGCCGCCTTA AGCTTCTAA ATTTGGAACA TCTAAGCAAG CTGAANGGAA AAGGGGTTT	240
CGCAAAATCA CTCGGGGAA NGGAAAGGTT GCTTTGTTAA TCATGCCCTA TGGTGGGTGA	300
TTAACTGCTT GTACAATTAC NTTTCACTTT TAATTAATTG TGCTNAANGC TTTAATTANA	360
CTTGGGGGTT CCCTCCCCAN ACCAACCCCN CTGACAAAAA GTGCCNGCCC TCAAATNATG	420
TCCCGGCNT CNTGAAACA CACNGNGAA NGTTCTCATT NTCCCCNCNC CAGGTNAAAA	480
TGAAGGGTTA CCATNTTAA CNCCACCTCC ACNTGGCENN GCCTGAATCC TCNAAAANCN	540
CCCTCAANCN AATTNCTNNG CCCCAGTCNC GCNTNNGTCC CNCCCGGGCT CCGGGAANTN	600
CACCCCCNGA ANNCCNTNNC NAACNAAATT CCGAAAATAT TCCCNNTCNC TCAATTCCCC	660
CNNAGACTNT CCTCNANCN CNCAATTTC TTTNNNTCAC GAACNCGNNC CNAAAATGN	720
NNNNCNCTC CNCTNGTCCN NAATCNCCAN C	751

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTGGTATTTT CTGTAAGATC AGGTGTTCCCT CCCTCGTAGG TTTAGAGGAA ACACCCTCAT	60
AGATGAAAAC CCCCCCGAGA CAGCAGCACT GCAACTGCCA AGCAGCCGGG GTAGGAGGGG	120
CGCCCTATGC ACAGCTGGGC CCTTGAGACA GCAGGGCTTC GATGTCAGGC TCGATGTCAA	180

TGGTCTGGAA	GCGGCGGCTG	TACCTGCGTA	GGGGCACACC	GTCAGGGCCC	ACCAGGAAC	240
TCTCAAAGTT	CCAGGCAACN	TCGTTGCGAC	ACACCGGAGA	CCAGGTGATN	AGCTTGGG	300
CGGTCTAAAN	CGCGGTGGCG	TCGTCGCTGG	GAGCTGGCAG	GGCCTCCGC	AGGAAGGCNA	360
ATAAAAGGTG	CGCCCCCGCA	CCGTTCANCT	CGCACTTCTC	NAANACCATG	ANGTTGGG	420
CNAACCCACC	ACCANNCCGG	ACTTCCTTGA	NGGAATTCCC	AAATCTCTTC	GNTCTTGGG	480
TTCTNCTGAT	GCCCTANCTG	GTTGCCNGN	ATGCCAANCA	NCCCCAANCC	CCGGGGTCCT	540
AAANCACCCN	CCTCCTCN	TCATCTGGGT	TNTNTCCCC	GGACCN	TCCCTCTCAAG	600
GGANCCATA	TCTCNACCAN	TACTCACCNT	NCCCCCCCNT	GNNACCCANC	CTTCTANN	660
TTCCCNCCCG	NCCTCTGGCC	CNTCAAANAN	GCTTNACNA	CCTGGGTCTG	CCTTCCCCC	720
TNCCCTATCT	GNACCCNCN	TTTGTCTCAN	TNT			753

## (2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 341 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACTATATCCA	TCACAACAGA	CATGCTTCAT	CCCATAGACT	TCTTGACATA	GCTTCAAATG	60
AGTGAACCCA	TCCTTGATT	ATATACATAT	ATGTTCTCAG	TATTTTGGGA	GCCTTCCAC	120
TTCTTAAAC	CTTGTTCATT	ATGAACACTG	AAAATAGGAA	TTTGTGAAGA	GTAAAAAGT	180
TATAGCTTGT	TTACGTAGTA	AGTTTTGAA	GTCTACATTC	AATCCAGACA	CTTAGTTGAG	240
TGTTAAACTG	TGATTTTAA	AAAATATCAT	TTGAGAATAT	TCTTCAGAG	GTATTTCAT	300
TTTACTTTT	TGATTAATTG	TGTTTATAT	ATTAGGGTAG	T		341

## (2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACTTACTGAA	TTTAGTTCTG	TGCTCTTCCT	TATTTAGTGT	TGTATCATAA	ATACTTTGAT	60
GTTTCAAACA	TTCTAAATAA	ATAATTTCA	GTGGCTTCAT	A		101

## (2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo spiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACATCTTGT TACAGTCTAA GATGTGTTCT TAAATCACCA TTCCCTCCTG GTCCTCACCC	60
TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTTACAGC AAATTAAGAT	120
TCAGATGCCT TGCTAAGTCT AGAGTTCTAG AGTTATGTTT CAGAAAGTCT AAGAAACCCA	180
CCTCTTGAGA GGTCAAGTAAA GAGGACTTAA TATTTCATAT CTACAAAATG ACCACAGGAT	240
TGGATACAGA ACGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACCTGCC CGGGGGCCGC	300
TCGAA	305

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACATAAAATAT CAGAGAAAAG TAGTCTTGA AATATTACG TCCAGGAGTT CTTTGTCTTCT	60
GATTATTTGG TGTGTGTTT GGTTTGTGTC CAAAGTATTG GCAGCTTCAG TTTTCATTTC	120
CTCTCCATCC TCGGGCATTG TTCCCAAATT TATATACCAAG TCTTCGTCCA TCCACACGCT	180
CCAGAATTTC TCTTTGTAG TAATATCTCA TAGCTCGGCT GAGCTTTCA TAGGTCATGC	240
TGCTGTTGTT CTTCTTTTA CCCCATAGCT GAGCCACTGC CTCTGATTTC AAGAACCTGA	300
AGACGCCCTC AGATCGGTCT TCCCATTGTTA TTAATCCTGG GTTCTTGTCT GGGTTCAAGA	360
GGATGTCGCG GATGAATTCC CATAAGTGAG TCCCTCTCGG GTTGTGCTTT TTGGTGTGGC	420
ACTTGGCAGG GGGGTCTTGC TCCTTTTCA TATCAGGTGA CTCTGCAACA GGAAGGTGAC	480
TGGTGGTTGT CATGGAGATC TGAGCCCGGC AGAAAGTTT GCTGTCCAAC AAATCTACTG	540
TGCTACCATA GTTGGTGTCA TATAAAATAGT TCTNGTCTTT CCAGGTGTTCA ATGATGGAAG	600
GCTCAGTTG TTCAGTCTTG ACAATGACAT TGTGTGTTGA CTGGAACAGG TCACTACTGC	660
ACTGGCCGTT CCACTTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCCG GCCGTCCCTG	720
CCGCCCGGGT GAACTCCTGC AAACATCATGC TGCAAAGGTG CTCGCCGTTG ATGTCGAAC	780
CNTGGAAAGG GATACAATTG GCATCCAGCT GGTTGGTGTCA CAGGAGGTGA TGGAGCCACT	840
CCCACACCTG GT	852

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAACAGACC CTTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCCG	60
AGTCTGACAC CATCCGGAGC ATCAGCATTG CTTCGCAGTG CCCTACCGCG GGGAACTCTT	120
GCCTCGTTTC TGGCTGGGGT CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCACTGCG	180

TGAACGTGTC GGTGGTGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT 234

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTTTTTATT TAAATGTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA	60
ATTTGATAGC AATATTTGG AGATTACAGA GTTTAGTAA TTACCAATTA CACAGTTAAA	120
AAGAAGATAA TATATTCAA GCANATACAA AATATCTAAT GAAAGATCAA GGCAGGAAAA	180
TGANTATAAC TAATTGACAA TGGAAAATCA ATTTTAATGT GAATTGCACA TTATCCTTAA	240
AAAGCTTCA AAANAAANAA TTATTGCAGT CTANTTAATT CAAACAGTGT TAAATGGTAT	300
CAGGATAAAAN AACTGAAGGG CANAAAGAAT TAATTTCAC TTCATGTAAC NCACCCANAT	360
TTACAATGGC TTAAATGCAN GGAAAAGCA GTGGAAGTAG GGAAGTANTC AAGGTCTTTC	420
TGGTCTCTAA TCTGCCTTAC TCTTGGGTG TGGCTTGAT CCTCTGGAGA CAGCTGCCAG	480
GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAAG GACACATGCT	540
GCCTTCCTTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT	590

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTAAAG AAGGAAAAAA AACGAGGCC	60
TGAACAGAAT TTTCCTGNAC AACGGGGCTT CAAAATAATT TTCTTGGGA GTTCAAGAC	120
GCTTCACTGC TTGAAACTTA AATGGATGTG GGACANAATT TTCTGTAATG ACCCTGAGGG	180
CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAG GGGACAAAGG CTAATCCAA	240
AACATCAAAG AAAGGAAGGT GGCGTCATAC CTCCCAGCCT ACACAGTTCT CCAGGGCTCT	300
CCTCATCCCT GGAGGACGAC AGTGGAGGAA CAACTGACCA TGTCCCCAGG CCTCTGTGTG	360
CTGGCTCCTG GTCTTCAGCC CCCAGCTCTG GAAGCCCACC CTCTGCTGAT CCTCGTGGC	420
CCACACTCCT TGAACACACA TCCCCAGGTT ATATTCTGG ACATGGCTGA ACCTCCTATT	480
CCTACTTCCG AGATGCCTTG CTCCCTGCAG CCTGTAAAA TCCCACTCAC CCTCCAAACC	540
ACGGCATGGG AAGCCTTCT GACTTGCTG ATTACTCCAG CATCTTGGAA CAATCCCTGA	600
TTCCCCACTC CTTAGAGGCA AGATAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC	660
AGGCTGCTGG CTTCAAATTN TGGCTCATT ACGAGCTATG GGACCTTGGG CAAGTNATCT	720
TCACTTCTAT GGGCNTCATT TTGTTCTACC TGCAAAATGG GGGATAATAA TAGT	774

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CANAAATTGA AATTTTATAA AAAGGCATTT TTCTCTTATA TCCATAAAAT GATATAATT	60
TTGCAANTAT ANAAATGTGT CATAAATTAT AATGTTCTT AATTACAGCT CAACGCAACT	120
TGGT	124

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCCGATGCTA CTATTTTATT GCAGGAGGTG GGGGTGTTTT TATTATTCTC TCAACAGCTT	60
TGTGGCTACA GGTGGTGTCT GACTGCATNA AAAANTTTT TACGGGTGAT TGCAAAAATT	120
TTAGGGCACC CATATCCCAA GCANTGT	147

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACATTAATT AATAAAAGGA CTGTTGGGT TCTGCTAAA CACATGGCTT GATATATTGC	60
ATGGTTTGAG GTTAGGAGGA GTTAGGCATA TGTTTGGGA GAGGGGT	107

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTCCTAGGAA GTCTAGGGAA CACACGACTC TGGGGTCACG GGGCCGACAC ACTTGACACGG	60
CGGGAAGGAA AGGCAGAGAA GTGACACCGT CAGGGGGAAA TGACAGAAAG GAAAATCAAG	120
GCCTTGCAAG GTCAGAAAGG GGACTCAGGG CTTCCACCAAC AGCCCTGCC CACTTGGCCA	180
CCTCCCTTTT GGGACCAGCA ATGT	204

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACAAAGATAA CATTATCTT ATAACAAAAA TTTGATAGTT TTAAAGGTTA GTATTGTGTA	60
GGGTATTTTC CAAAAGACTA AAGAGATAAC TCAGGTAAAA AGTTAGAAAT GTATAAAACA	120
CCATCAGACA GGTTTTAAA AAACAAACATA TTACAAAATT AGACAATCAT CCTTAAAAAA	180
AAAACCTTCTT GTATCAATT TTGTTGTTCA AAATGACTGA CTTAANTATT TTTAAATATT	240
TCANAAACAC TTCCTCAAAA ATTTCAANA TGGTAGCTTT CANATGTNCC CTCAGTCCC	300
ATGTTGCTCA GATAAATAAA TCTCGTGAGA ACTTACCAACC CACCACAAGC TTTCTGGGC	360
ATGCAACAGT GTCTTTCTT TNCTTTTCTT TTTTTTTTT TTACAGGCAC AGAAACTCAT	420
CAATTATTATT TGGATAACAA AGGGTCTCCA AATTATATTG AAAAATAAAT CCAAGTTAAT	480
ATCACTCTG T	491

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACATAATTAA GCAGGGCTAA TTACCATAG ATGCTATTAA TTAANAGGTN TATGATCTGA	60
GTATTAACAG TTGCTGAAGT TTGGTATTTT TATGCAGCAT TTTCTTTTG CTTTGATAAC	120
ACTACAGAAC CCTTAAGGAC ACTGAAAATT AGTAAGTAAA GTTCAGAAC ATTAGCTGCT	180
CAATCAAATC TCTACATAAC ACTATAGTAA TTAAAACGTT AAAAAAAAGT GTTGAATCT	240
GCACTAGTAT ANACCGCTCC TGTCAGGATA ANACTGCTTT GGAACAGAAA GGGAAAANC	300
AGCTTGANT TTCTTTGTGC TGATANGAGG AAAGGCTGAA TTACCTTGTT GCCTCTCCCT	360
AATGATTGGC AGGTCNGGTAA ATNCCAAAA CATATTCCAA CTCAACACTT CTTTTCCNCG	420
TANCTTGANT CTGTGTATTC CAGGANCAGG CGGATGGAAT GGGCCAGCCC NC GGATGTTCA	480
CANT	484

## (2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACTAAACCTC GTGCTTGTGA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG	60
CCACTGGGTA TACTGCTGAC AACCGCAACA ACAAAAACAC AAATCCTTGG CACTGGCTAG	120
TCTATGTCCT CTCAAGTGCC TTTTTGTTTG T	151

## (2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACCTGGCTTG TCTCCGGGTG GTTCCCGGCG CCCCCCACGG TCCCCAGAAC GGACACTTTC	60
GCCCTCCAGT GGATACTCGA GCCAAAGTGG T	91

## (2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCGGATGTG CGTTGGTTAT ATACAAATAT GTCATTTAT GTAAGGGACT TGAGTATACT	60
TGGATTTTG GTATCTGTGG GTTGGGGGGA CGGTCCAGGA ACCAATACCC CATGGATACC	120
AAGGGACAAAC TGT	133

## (2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGGATGA GGTGATGCAN GCNGTGGCGC  
 GACTGGGAGC TGAGCCCTTC CCTTTGCGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA  
 TCTCANTGGG CTGGATNCAT GCAGGGT

60  
 120  
 147

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGTAAAATAC ATTGAATTTT CTGTATACTC  
 TGATTACATA CATTATCCT TTAAAAAAGA TGTAAATCTT AATTTTTATG CCATCTATTA  
 ATTTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACTGAATT TAACTAGTT  
 TTGACTTCTA AGTTGGT

60  
 120  
 180  
 198

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAACAAATG GGTTGTGAGG AAGTCTTATC AGCAAAACTG GTGATGGCTA CTGAAAAGAT  
 CCATTGAAAA TTATCATTAA TGATTTAAA TGACAAAGTTA TCAAAAACTC ACTCAATTTC  
 CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA  
 TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG  
 CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT  
 TTTCGTCTTT ATTGGACTTC TTTGAAGAGT

60  
 120  
 180  
 240  
 300  
 330

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTACTTCGGC 60  
GTCGTGGGCT CCTTCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCGCAC 120  
TCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGCG ATTCCCGTGC CTGGT 175

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 154 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACCCCACTTT TCCTCCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT 60  
GGTTGTTGCT CTTCAACAGT ATCCTCCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC 120  
TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT 154

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGCTCGAGCC CTATAGTGAG TCGTATTAGA 30

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 89 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACAAGTCATT TCAGCACCCCT TTGCTCTTCA AAACTGACCA TCTTTATAT TTAATGCTTC  
CTGTATGAAT AAAAATGGTT ATGTCAAGT

60  
89

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA GGTTCTGCAG  
AATCAGTGCA TCCAGGATTG GTCCTGGAT CTGGGGT

60  
97

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ACAACAANAA NTCCCTTCTT TAGGCCACTG ATGGAACCT GGAACCCCT TTTGATGGCA  
GCATGGCGTC CTAGGCCTTG ACACAGCGGC TGGGTTTGG GCTNTCCAA ACCGCACACC  
CCAACCCTGG TCTACCCACA NTTCTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT  
TCGGTCATAA NATGAAATCC CAANGGGAC AGAGGTCAGT AGAGGAAGCT CAATGAGAAA  
GGTGCTGTT GCTCAGCCAG AAAACAGCTG CCTGGCATTC GCCGCTGAAC TATGAACCCG  
TGGGGGTGAA CTACCCCCAN GAGGAATCAT GCCTGGCGA TGCAANGGTG CCAACAGGAG  
GGCGGGGAGG AGCATGT

60  
120  
180  
240  
300  
360  
377

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACGCCTTCC	CTCAGAATT	AGGGAAGAGA	CTGTCGCC	CCTTCCTCC	TTGTTGCG	60
AGAACCCGT	TGCCCCTT	CACCATATCC	ACCCTCGC	CATCTTGAA	CTCAAACACG	120
AGGAACTAAC	TGCACCCTG	TCCTCTCCC	AGTCCCAGT	TCACCCTCC	TCCCTCACCT	180
TCCTCCACTC	TAAGGGATAT	CAACACTGCC	CAGCACAGGG	GCCCTGAATT	TATGTGGTT	240
TTATATATTT	TTTAATAAGA	TGCACTTTAT	GTCATTTT	AATAAAGTCT	GAAGAATTAC	300
						305
TGTTT						

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACTACACACA	CTCCACTTGC	CCTTGTGAGA	CACTTTGTCC	CAGCACTTTA	GGAATGCTGA	60
GGTCGGACCA	GCCACATCTC	ATGTGCAAGA	TTGCCAGCA	GACATCAGGT	CTGAGAGTTC	120
CCCTTTAAA	AAAGGGGACT	TGCTTAAAAAA	AGAAGTCTAG	CCACGATTGT	GTAGAGCAGC	180
TGTGCTGTGC	TGGAGATTCA	CTTTGAGAG	AGTTCTCCTC	TGAGACCTGA	TCTTTAGAGG	240
CTGGGCAGTC	TTGCACATGA	GATGGGGCTG	GTCTGATCTC	AGCACTCCTT	AGTCTGCTTG	300
CCTCTCCCAG	GGCCCCAGCC	TGGCCACACC	TGCTTACAGG	GCACTCTCAG	ATGCCCATAC	360
CATAGTTCT	GTGCTAGTGG	ACCGT				385

## (2) INFORMATION FOR SEQ ID NO:68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ACTTAACCAG	ATATATTTT	ACCCCAGATG	GGGATATTCT	TTGTAAAAAA	TGAAAATAAA	60
GTTTTTTAA	TGG					73

## (2) INFORMATION FOR SEQ ID NO:69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGGGCTC	TCACCCTCCT	CTCCTGCAGC	60
TCCAGCTTTG	TGCTCTGCCT	CTGAGGAGAC	CATGGCCAG	CATCTGAGTA	CCCTGCTGCT	120
CCTGCTGGCC	ACCCTAGCTG	TGGCCCTGGC	CTGGAGCCCC	AAGGAGGAGG	ATAGGATAAT	180
CCCGGGTGGC	ATCTATAACG	CAGACCTCAA	TGATGAGTGG	GTACAGCGTG	CCCTTCACTT	240
CGCCATCAGC	GAGTATAACA	AGGCCACCAA	AGATGACTAC	TACAGACGTC	CGCTGCGGGT	300
ACTAAGAGCC	AGGCAACAGA	CCGTTGGGGG	GGTGAATTAC	TTCTTCGACG	TAGAGGTGGG	360
CCGAACCATA	TGTACCAAGT	CCCAGCCAA	CTTGGACACC	TGTGCCTTCC	ATGAACAGCC	420
AGAACTGCAG	AAGAAACAGT	TGTGCTCTT	CGAGATCTAC	GAAGTCCCT	GGGGAGAACAA	480
GAANGTCCCT	GGGTGAAATC	CAGGTGTCAA	GAAATCCTAN	GGATCTGTTG	CCAGGC	536

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGACCCCTA	ACAGGGGCC	TCTCAGCCCT	CCTAATGACC	TCCGGCCTAG	CCATGTGATT	60
TCACTTCCAC	TCCATAACGC	TCCTCATACT	AGGCCTACTA	ACCAACACAC	TAACCATATA	120
CCAATGATGG	CGCGATGTAA	CACGAGAAAG	CACATACCAA	GGCCACCACA	CACCACCTGT	180
CCAAAAAGGC	CTTCGATACG	GGATAATCCT	ATTTATTACC	TCAGAAGTTT	TTTTCTTCGC	240
AGGGATTTTT	CTGAGCCTTT	TACCACTCCA	GCCTAGCCCC	TACCCCCCAA	CTAGGAGGGC	300
ACTGGCCCCC	AACAGGCATC	ACCCCGCTAA	ATCCCCTAGA	AGTCCCACTC	CTAAACACAT	360
CCGTATTACT	CGCATCAGGA	GTATCAATCA	CCTGAGCTCA	CCATAGTCTA	ATAGAAAACA	420
ACCGAAACCA	AATTATTCAA	AGCACTGCTT	ATTACAATT	TACTGGGTCT	CTATT	477

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AGAGCTATAG	GTACAGTGTG	ATCTCAGCTT	TGCAAACACA	TTTTCTACAT	AGATAGTACT	60
AGGTATTAAT	AGATATGTAA	AGAAAGAAAT	CACACCATT	ATAATGGTAA	GATTGGTTA	120
TGTGATTTA	GTGGTATTTT	TGGCACCCCT	ATATATGTT	TCAAACATT	CAGCAGTGAT	180
ATTATTTC	AACTTAAAAA	AGTGAGTTG	AAAAAGAAAA	TCTCCAGCAA	GCATCTCATT	240
TAAATAAAGG	TTTGTATCT	TTAAAATAC	AGCAATATGT	GACTTTTAA	AAAAGCTGTC	300
AAATAGGTGT	GACCCTACTA	ATAATTATTA	GAAATACATT	TAAAACATC	GAGTACCTCA	360
AGTCAGTTG	CCTTGAAAAA	TATCAAATAT	AACTCTTAGA	GAAATGTACA	AAAAAGAATG	420
CTTCGTAATT	TTGGAGTANG	AGGTTCCCTC	CTCAATT	TATTTTAAA	AAGTACATGG	480

TAAAAAAAAA AATTACACAAC AGTATATAAG GCTGTAAAAT GAAGAATTCT GCC 533

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TATTACGGAA AAACACACCA CATAATTCAA CTANCAAAGA ANACTGCTTC AGGGCGTGTA	60
AAATGAAAGG CTTCCAGGCA GTTATCTGAT TAAAGAACAC TAAAAGAGGG ACAAGGCTAA	120
AAGCCGCAGG ATGTCTACAC TATANCAGGC GCTATTGGG TTGGCTGGAG GAGCTGTGGA	180
AAACATGGAN AGATTTGGTC TGGANATCGC CGTGGCTATT CCTCATTGTT ATTACANAGT	240
GAGGTTCTCT GTGTGCCAC TGGTTTGAAA ACCGTTCTNC AATAATGATA GAATAGTACA	300
CACATGAGAA CTGAAATGGC CCAAACCCAG AAAGAAAGCC CAACTAGATC CTCAGAANAC	360
GCTTCTAGGG ACAATAACCG ATGAAGAAAA GATGGCCTCC TTGTGCCCTC GTCTGTTATG	420
ATTTCTCTCC ATTGCAGCNA NAAACCCGTT CTTCTAAGCA AACNCAGGTG ATGATGGCNA	480
AAATACACCC CCTCTTGAAG NACCNGGAGG A	511

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAGTGCCAGC ACTGGTGCCA GTACCAAGTAC CAATAACAGT GCCAGTGCCA GTGCCAGCAC	60
CAGTGGTGGC TTCAGTGCTG GTGCCAGCCT GACCGCCACT CTCACATTTG GGCTCTTCGC	120
TGGCCTTGGT GGAGCTGGTG CCAGCACCAAG TGGCAGCTCT GGTGCCTGTG GTTTCTCCTA	180
CAAGTGAGAT TTTAGATATT GTTAATCCTG CCAGTCTTC TCTTCAAGCC AGGGTGCATC	240
CTCAGAAACC TACTCAACAC AGCACTCTAG GCAGCCACTA TCAATCAATT GAAGTTGACA	300
CTCTGCATTA AATCTATTTG CCATTCTGA AAAAAAAA AAAAAAAGGG CGGCCGCTCG	360
ANTCTAGAGG GCCCGTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT ANTTGCCAGC	420
CATCTGTTGT TTGCCCTC CCCGNTGCCT TCCTTGACCC TGGAAAGTGC CACTCCACT	480
GTCCTTCCT AANTAAAAT	499

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

TTTCATAGGA	GAACACACTG	AGGAGATACT	TGAAGAATT	GGATTCA	GCGAAGAGAT	60
TTATCAGCTT	AACTCAGATA	AAATCATTGA	AAGTAATAAG	GTAAAAGCTA	GTCTCTAA	120
TCCAGGCCA	CGGCTCAAGT	GAATTGAA	ACTGCATT	CAGTGTAGAG	TAACACATAA	180
CATTGTATGC	ATGGAAACAT	GGAGGAACAG	TATTACAGTG	TCCTACC	CTAATCAAGA	240
AAAGAATTAC	AGACTCTGAT	TCTACAGTG	TGATTGAATT	CTAAAATGG	TAATCATTAG	300
GGCTTTGAT	TTATAANACT	TTGGGTACTT	ATACTAAATT	ATGGTAGTTA	TA	360
CAGTTGCTT	GATATATTG	TTGATATTAA	GATTCTTGAC	TTATATT	TTG AATGGGTTCT	420
ACTGAAAAAN	GAATGATATA	TTCTTGAAGA	CATCGATATA	CATTATT	TTA CACTCTTGAT	480
TCTACAATGT	AGAAAATGAA	GGAAATGCC	CAAATTGTAT	GGTGATA	AAA GTCCCGT	537

## (2) INFORMATION FOR SEQ ID NO: 75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CAAANACAAT	TGTTCAAAAG	ATGCAAATGA	TACACTACTG	CTGCAGCTA	CAAACACCTC	60
TGCATATTAC	ACGTACCTCC	TCCTGCTCCT	CAAGTAGTGT	GGTCTATT	TTT GCCATCATCA	120
CCTGCTGTCT	GCTTAGAAGA	ACGGCTTTCT	GCTGCAANGG	AGAGAAATCA	TAACAGACGG	180
TGGCACAAAGG	AGGCCATCTT	TTCCTCATCG	GTTATTGTCC	CTAGAACCGT	CTTCTGAGGA	240
TCTAGTTGGG	CTTTCTTCT	GGGTTGGGC	CATTCANTT	CTCATGTGTG	TACTATTCTA	300
TCATTATTGT	ATAACGGTTT	TCAAACCNGT	GGGCACNCAG	AGAACCTCAC	TCTGTAATAA	360
CAATGAGGAA	TAGCCACGGT	GATCTCCAGC	ACCAAATCTC	TCCATGTTNT	TCCAGAGCTC	420
CTCCAGCCAA	CCCAAATAGC	CGCTGCTATN	GTGTAGAAC	A TCCCTGN		467

## (2) INFORMATION FOR SEQ ID NO: 76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

AAGCTGACAG	CATTGGGCC	GAGATGTCTC	GCTCCGTGGC	CTTAGCTGTG	CTCGCGCTAC	60
TCTCTCTTTC	TGGCCTGGAG	GCTATCCAGC	GTACTCCAAA	GATTCA	GGTT TACTCACGTC	120
ATCCACGAGA	GAATGGAAAG	TCAAATTCC	TGAATTGCTA	TGTGTCTGGG	TTTCATCCAT	180
CCGACATTGA	AGTTGACTTA	CTGAAGAATG	GAGAGAGAAT	TGAAAAGTG	GAGCATT	240
ACTTGTCTTT	CAGCAAGGAC	TGGTCTTCT	ATCTCTGTA	CTACACTGAA	TTCACCCCCA	300
CTGAAAAAGA	TGAGTATGCC	TGCCGTGTGA	ACCATGTGAC	TTTGTACAG	CCCAGATNG	360

TTNAGTGGGA TCGANACATG TAAGCAGCAN CATGGGAGGT 400

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGGAGTGCC TTGGTGTTC AAGCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT	60
CCAGCTGCC CGGCGGGGGA TGCGAGGCTC GGAGCACCCCT TGCCCGGCTG TGATTGCTGC	120
CAGGCACTGT TCATCTCAGC TTTCTGTCC CTTTGCTCCC GGCAAGCGCT TCTGCTGAAA	180
GTTCATATCT GGAGCCTGAT GTCTTAACGA ATAAAGGTCC CATGCTCCAC CCGAAAAAAA	240
AAAAAAA	248

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCAA CACAATGGCT ACCTTTAACAA	60
TCACCCAGAC CCCGCCCTGC CCGTGCCCCA CGCTGCTGCT AACGACAGTA TGATGCTTAC	120
TCTGCTACTC GGAAACTATT TTTATGTAAT TAATGTATGC TTTCTTGTAA ATAAATGCCT	180
GATTAAAAAA AAAAAAAA A	201

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCTTTGTT AGGTTTTGA GACAACCCTA GACCTAACT GTGTCACAGA CTTCTGAATG	60
TTTAGGCAGT GCTAGTAATT TCCTCGTAAT GATTCTGTTA TTACTTCCCT ATTCTTATT	120
CCTCTTCTT CTGAAGATTA ATGAAGTTGA AAATTGAGGT GGATAAATAC AAAAAGGTAG	180

TGTGATAGTA	TAAGTATCTA	AGTGCAGATG	AAAGTGTGTT	ATATATATCC	ATTCAAAATT	240
ATGCAAGTTA	GTAAATTACTC	AGGGTTAACT	AAATTACTTT	AATATGCTGT	TGAACCTACT	300
CTGTTCTTG	GCTAGAAAAA	ATTATAAACCA	GGACTTTGTT	AGTTGGGAA	GCCAAATTGA	360
TAATATTCTA	TGTTCTAAAA	GTTGGGCTAT	ACATAAANTA	TNAAGAAATA	TGGAATTTTA	420
TTCCCAGGAA	TATGGGGTTC	ATTTATGAAT	ANTACCCGGG	ANAGAAGTTT	TGANTNAAAC	480
CNGTTTGGT	TAATACGTTA	ATATGTCCTN	AATNAACAAG	GCNTGACTTA	TTTCCAAAAAA	540
AAAAAAAAAA	AA					552

## (2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 476 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGGGATT	GAGATGCTAA	GGCCCCAGAG	ATCGTTGAT	CCAACCCTCT	TATTTTCAGA	60
GGGGAAAATG	GGGCCTAGAA	GTTACAGAGC	ATCTAGCTGG	TGCGCTGGCA	CCCCTGGCCT	120
CACACAGACT	CCCGAGTAGC	TGGGACTACA	GGCACACAGT	CACTGAAGCA	GGCCCTGTTT	180
GCAATTCA	CGTTGACCTC	CAACTTAAAC	ATTCTTCATA	TGTGATGTCC	TTAGTCACTA	240
AGGTTAAACT	TTCCCACCCA	GAAAAGGCAA	CTTAGATAAA	ATCTTAGAGT	ACTTTCATAC	300
TCTTCTAAGT	CCTCTTCCAG	CCTCACTTG	AGTCCTCCTT	GGGGGTTGAT	AGGAANTNTC	360
TCTTGGCTTT	CTCAATAAAA	TCTCTATCCA	TCTCATGTTT	AATTTGGTAC	GCNTAAAAAT	420
GCTGAAAAAA	TTAAAATGTT	CTGGTTTCNC	TTTAAAAAAA	AAAAAAA	AAAAAA	476

## (2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 232 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTTTTTTTTG	TATGCCNTCN	CTGTGGNGTT	ATTGTTGCTG	CCACCCCTGGA	GGAGCCCAGT	60
TTCTTCTGTA	TCTTTCTTTT	CTGGGGGATC	TTCCTGGCTC	TGCCCCCTCCA	TTCCCAGCCT	120
CTCATCCCCA	TCTTGCACTT	TTGCTAGGGT	TGGAGGGCGCT	TTCTGGTAG	CCCCTCAGAG	180
ACTCAGTCAG	CGGGAATAAG	TCCTAGGGT	GGGGGGTGTG	GCAAGCCGGC	CT	232

## (2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 383 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGGCGGGAGC AGAAGCTAAA GCCAAAGCCC AAGAAGAGTG GCAGTGCCAG CACTGGTGCC	60
AGTACCACTA CCAATAACAT GCCAGTGCCA GTGCCAGCAC CAGTGGTGGC TTCAGTGCTG	120
GTGCCAGCCT GACCGCCACT CTCACATTTG GGCTCTTCGC TGGCCTTGGT GGAGCTGGTG	180
CCAGCACCAG TGGCAGCTCT GGTGCCTGTG GTTTCTCCTA CAAGTGAGAT TTTAGATATT	240
GTAAATCCTG CCAGTCTTTC TCTTCAAGCC AGGGTGCATC CTCAGAAACC TACTCAACAC	300
AGCACTCTNG GCAGCCACTA TCAATCAATT GAAGTTGACA CTCTGCATTA AATCTATTTG	360
CCATTTCAAA AAAAAAAA AAA	383

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 494 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTCCTC CAGTATTACC TCAACGAGCA	60
GGGAGATCGA GTCTATACGC TGAAGAAATT TGACCCGATG GGACAAACAGA CCTGCTCAGC	120
CCATCCTGCT CGGTTCTCCC CAGATGACAA ATACTCTCGA CACCGAATCA CCATCAAGAA	180
ACGCTTCAAG GTGCTCATGA CCCAGCAACC GCGCCCTGTC CTCTGAGGGT CCTTAAACTG	240
ATGTCTTTTC TGCCACCTGT TACCCCTCGG AGACTCCGTA ACCAAACTCT TC GGACTGTG	300
AGCCCTGATG CCTTTTGCC AGCCATACTC TTTGGCNTCC AGTCTCTCGT GGCGATTGAT	360
TATGCTTGTG TGAGGCAATC ATGGTGGCAT CACCCATNAA GGGAACACAT TTGANTTTT	420
TTTCNCATAT TTTAAATTAC NACCAGAATA NTTCAGAATA AATGAATTGA AAAACTCTTA	480
AAAAAAA AAAA	494

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTGGTAGCC TATGGCGTGG CCACGGGANGG GCTCCTGAGG CACGGGACAG TGACTTCCCA	60
AGTATCCTGC GCCCGTCTT CTACCGTCCC TACCTGCAGA TCTTCGGGCA GATTCCCCAG	120
GAGGACATGG ACGTGGCCCT CATGGAGCAC AGCAACTGCT CGTCGGAGCC CGGCTTCTGG	180
GCACACCCTC CTGGGGCCCA GGCGGGCACC TGCGTCTCCC AGTATGCCAA CTGGCTGGTG	240
GTGCTGCTCC TCGTCATCTT CCTGCTCGTG GCCAACATCC TGCTGGTCAC TTGCTCATTG	300
CCATGTTCAAG TTACACATTC GGCAAAGTAC AGGGCAACAG CNATCTCTAC TGGGAAGGCC	360
AGCGTTNCCG CCTCATCCGG	380

## (2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAGTTAGCTC	CTCCACAAACC	TTGATGAGGT	CGTCTGCAGT	GGCCTCTCGC	TTCATACCGC	60
TNCCATCGTC	ATACTGTAGG	TTTGCCACCA	CCTCCTGCAT	CTTGGGGCGG	CTAATATCCA	120
GGAAACTCTC	AATCAAGTCA	CCGTCNATNA	AACCTGTGGC	TGGTTCTGTC	TTCCGCTCGG	180
TGTGAAAGGA	TCTCCAGAAG	GAGTGCTCGA	TCTTCCCCAC	ACTTTGATG	ACTTTATTGA	240
GTCGATTCTG	CATGTCCAGC	AGGAGGTTGT	ACCAGCTCTC	TGACAGTGAG	GTCACCAGCC	300
CTATCATGCC	NTTGAACGTG	CCGAAGAACAA	CCGAGCCTTG	TGTGGGGGGT	GNAGTCTCAC	360
CCAGATTCTG	CATTACCAGA	NAGCCGTGGC	AAAAGANATT	GACAACCTCGC	CCAGGNNNGAA	420
AAAGAACACC	TCCTGGAAGT	GCTNGCCGCT	CCTCGTCCNT	TGGTGGNNNGC	GCNTNCCTTT	480
T						481

## (2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGATN	TTGTCTGCTG	AGAATTCA	60
ACTTGAAAAA	GCAACTTNAA	GCCTGGACAC	TGGTATTAAA	ATTCAACAATA	TGCAACACTT	120
TAAACAGTGT	GTCAATCTGC	TCCCTTACTT	TGTCATCACC	AGTCTGGAA	TAAGGGTATG	180
CCCTATTACAC	ACCTGTTAAA	AGGGCGCTAA	GCATTTTGA	TTCAACATCT	TTTTTTTGA	240
CACAAGTCCG	AAAAAAAGCAA	AAGTAAACAG	TTNTTAATTT	GTTAGCCAAT	TCACTTCTT	300
CATGGGACAG	AGCCATTGTA	TTTAAAAAGC	AAATTGCATA	ATATTGAGCT	TTGGGAGCTG	360
ATATNTGAGC	GGAAGANTAG	CCTTCTACT	TCACCAGACA	CAACTCCTT	CATATTGGGA	420
TGTTNACNAA	AGTTATGTCT	CTTACAGATG	GGATGCTTT	GTGGCAATT	TG	472

## (2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AGAAACCAGT ATCTCTNAAA ACAACCTCTC ATACCTTGTG GACCTAATTT TGTGTGCGTG	60
TGTGTGTGCG CGCATATTAT ATAGACAGGC ACATCTTTT TACTTTGTA AAAGCTTATG	120
CCTCTTGCT ATCTATATCT GTGAAAGTTT TAATGATCTG CCATAATGTC TTGGGGACCT	180
TTGTCTTCTG TGAAATGGT ACTAGAGAAA ACACCTATNT TATGAGTCAA TCTAGTTNGT	240
TTTATTCGAC ATGAAGGAAA TTTCCAGATN ACAACACTNA CAAACTCTCC CTTGACTAGG	300
GGGGACAAAG AAAAGCANAA CTGAACATNA GAAACAATTN CCTGGTGAGA AATTNCATAA	360
ACAGAAATTG GGTNGTATAT TGAAANANNG CATCATTNAA ACGTTTTTT TTT	413

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CGCAGCGGGT CCTCTCTATC TAGCTCCAGC CTCTCGCCTG CCCCACCTCCC CGCGTCCCGC	60
GTCCTAGCCN ACCATGGCCG GGCCCCCTGCG CGCCCCCGCTG CTCCTGCTGG CCATCCTGGC	120
CGTGGCCCTG GCCGTGAGCC CCGCGGCCGG CTCCAGTCCC GGCAAGCCGC CGCGCCTGGT	180
GGGAGGCCA TGGACCCCGC GTGGAAGAAG AAGGTGTGCG GCGTGCAGTG GACTTTGCCG	240
TCGGCNANTA CAACAAACCC GCAACNACTT TTACCNAGCN CGCGCTGCAG GTTGTGCCGC	300
CCCAANCAA TTGTACTNG GGGTAANTAA TTCTTGAAG TTGAACCTGG GCCAAACNNG	360
TTTACCAAGAA CCNAGCCAAT TNGAACATT NCCCCTCCAT AACAGCCCCT TTTAAAAAGG	420
GAANCANTCC TGNTCTTTTC CAAATTAA	448

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTTGTG CACTGGCCAC TGTGATGGAA CCATTGGCC AGGATGCTTT GAGTTTATCA	60
GTAGTGATTG TGCCAAAGTT GGTGTTGTA CATGAGTATG TAAAATGTCA AAAAATTAGC	120
AGAGGTCTAG GTCTGCATAT CAGCAGACAG TTTGTCCGTG TATTTGTAG CCTTGAAGTT	180
CTCAGTGACA AGTNNNTCT GATGCGAAGT TCTNATTCCA GTGTTTAGT CCTTGCATC	240
TTTNATGTT AGACTTGCCT CTNTNAAATT GCTTTGTNT TCTGCAGGTA CTATCTGTGG	300
TTAACAAAA TAGAANNACT TCTCTGCTTN GAANATTGA ATATCTTACA TCTNAAAATN	360
AATTCTCTCC CCATANAAA ACCCANGCCC TTGGGANAAT TTGAAAANG GNTCCTTCNN	420
AATTCCNNANA ANTTCAGNTN TCATACAACA NAACNGGANC CCC	463

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AGGGATTGAA	GGTCTNTTNT	ACTGTCGGAC	TGTTCANCCA	CCAACTCTAC	AAGTTGCTGT	60
CTTCCACTCA	CTGTCGTAA	GCNTNTTAAC	CCAGACTGTA	TCTTCATAAA	TAGAACAAAT	120
TCTTCACCAAG	TCACATCTTC	TAGGACCTTT	TTGGATTCAAG	TTAGTATAAG	CTCTTCCACT	180
TCCTTTGTTA	AGACTTCATC	TGGTAAAGTC	TTAAGTTTG	TAGAAAGGAA	TTTAATTGCT	240
CGTTCTCTAA	CAATGTCCTC	TCCTTGAAGT	ATTTGGCTGA	ACAACCCACC	TNAAGTCCT	300
TTGTGCATCC	ATTTTAAATA	TACTTAATAG	GGCATTGGTN	CACTAGGTTA	AATTCTGCAA	360
GAGTCATCTG	TCTGCAAAAG	TTGCGTTAGT	ATATCTGCCA			400

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 480 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAGCTCGGAT	CCAATAATCT	TTGTCTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCCTCTTT	GACTACCGTG	TGCCAGTGCT	GGTGATTCTC	ACACACCTCC	NNCCGCTCTT	180
TGTGGAAAAAA	CTGGCACTTG	NCTGGAACTA	GCAAGACATC	ACTTACAAAT	TCACCCACGA	240
GACACTTGAA	AGGTGTAACA	AAGCGACTCT	TGCATTGCTT	TTTGTCCCTC	CGGCACCAGT	300
TGTCAATACT	AACCCGCTGG	TTTGCCTCCA	TCACATTGT	GATCTGTAGC	TCTGGATACA	360
TCTCCTGACA	GTACTGAAGA	ACTTCTTCTT	TTGTTTCAA	AGCAACTCTT	GGTGCCTGTT	420
NGATCAGGTT	CCCATTTCCC	AGTCCGAATG	TTCACATGGC	ATATNTTACT	TCCCACAAAA	480

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 477 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATACAGCCC	NATCCCACCA	CGAAGATGCG	CTTGTGACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCCTG	TAGCCCCAGC	GACTCTCCAC	CTGCTGGAAG	CGGTTGATGC	TGCACTCCTT	120
CCCACGCAGG	CAGCAGCGGG	GCCGGTCAAT	GAACCTCCACT	CGTGGCTTGG	GGTTGACGGT	180
TAANTGCAGG	AAGAGGCTGA	CCACCTCGCG	GTCCACCAGG	ATGCCCGACT	GTGCGGGACC	240
TGCAGCGAAA	CTCCTCGATG	GTCATGAGCG	GGAAGCGAAT	GANGCCCAGG	GCCTTGCCCA	300
GAACCTTCCG	CCTGTTCTCT	GGCGTCACCT	GCAGCTGCTG	CCGCTNACAC	TCGGCCTCGG	360
ACCAGCGGAC	AAACGGCGTT	GAACAGCCGC	ACCTCACCGA	TGCCCANTGT	GTGCGCTCC	420
AGGAACGGCN	CCAGCGTGTC	CAGGTCAATG	TCGGTGAANC	CTCCGCGGGT	AATGGCG	477

## (2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAACGGCTGG	ACCTTGCCTC	GCATTGTGCT	GCTGGCAGGA	ATACCTTGGC	AAGCAGCTCC	60
AGTCCGAGCA	GCCCCAGACC	GCTGCCGCCC	GAAGCTAACG	CTGCCTCTGG	CCTTCCCCCTC	120
CGCCTCAATG	CAGAACCAANT	AGTGGGAGCA	CTGTGTTTAG	AGTTAACAGT	GAACACTGTN	180
TGATTTACT	TGGGAATTTC	CTCTGTTATA	TAGCTTTCC	CAATGCTAAT	TTCCAAACAA	240
CAACAAACAAA	ATAACATGTT	TGCCTGTTNA	GTTGTATAAA	AGTANGTGAT	TCTGTATNTA	300
AAGAAAATAT	TACTGTTACA	TATACTGCTT	GCAANTTCTG	TATTTATTGG	TNCTCTGGAA	360
ATAAAATATAT	TATTAAA					377

## (2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCCTTGAGG	GGTTAGGGTC	CAGTCCCCAG	TGGAAGAAC	AGGCCAGGAG	AANTGCGTGC	60
CGAGCTGANG	CAGATTTCCC	ACAGTGACCC	CAGAGCCCTG	GGCTATAGTC	TCTGACCCCT	120
CCAAGGAAAG	ACCACCTTCT	GGGGACATGG	GCTGGAGGGC	AGGACCTAGA	GGCACCAAGG	180
GAAGGCCCA	TTCCGGGGCT	GTTCCCCGAG	GAGGAAGGGA	AGGGGCTCTG	TGTCCCCCCC	240
ACGAGGAANA	GGCCCTGANT	CCTGGGATCA	NACACCCCTT	CACGTGTATC	CCCACACAAA	300
TGCAAGCTCA	CCAAGGTCCC	CTCTCAGTCC	CTTCCCTACA	CCCTGAACGG	NCACTGGCCC	360
ACACCCACCC	AGANCANCCA	CCCGCCATGG	GGAATGTNCT	CAAGGAATCG	CNGGGCAACG	420
TGGACTCTNG	TCCCNNAAAGG	GGGCAGAATC	TCCAATAGAN	GGANNGAAC	CTTGCTNANA	480
AAAAAAAANA	AAAAAA					495

## (2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGTTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACCATT	TTGTCTGCTC	60
CCTCTGGAAG	CCTTGCAG	AGCGGACTTT	GTAATTGTTG	GAGAATAACT	GCTGAATT	120
TAGCTGTTT	GAGTTGATT	GCACCACTGC	ACCACAACTC	AATATGAAAA	CTATTTNACT	180
TATTATTAT	CTTGTGAAAA	GTATACAATG	AAAATTTGT	TCATACTGTA	TTTATCAAAGT	240
ATGATGAAAA	GCAATAGATA	TATATTCTTT	TATTATGTTN	AATTATGATT	GCCATTATTA	300
ATCGGCAAAA	TGTGGAGTGT	ATGTTCTTT	CACAGTAATA	TATGCCTTT	GTAACCTTCAC	360
TTGGTTATTT	TATTGTAAAT	GAATTACAAA	ATTCTTAATT	TAAGAAAATG	GTANGTTATA	420
TTTANTTCAN	TAATTTCTTT	CCTTGTAC	GTTAATT	AAAAGAATGC	AT	472

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTGAAGCATT	TCTTCAAAC	TNTCTACTTT	TGTCATTGAT	ACCTGTAGTA	AGTTGACAAT	60
GTGGTGAAAT	TTCAAAATT	TATGTAAC	CTACTAGTT	TACTTCTCC	CCCAAGTCTT	120
TTTTAACTCA	TGATTTTAC	ACACACAATC	CAGAACTTAT	TATATAGCCT	CTAAGTCTT	180
ATTCTTCACA	GTAGATGATG	AAAGAGTCCT	CCAGTGTCTT	GNGCANAATG	TTCTAGNTAT	240
AGCTGGATAC	ATACNGTGGG	AGTTCTATAA	ACTCATACCT	CAGTGGGACT	NAACCAAAAT	300
TGTGTTAGTC	TCAATTCTCA	CCACACTGAG	GGAGCCTCCC	AAATCACTAT	ATTCTTATCT	360
GCAGGGTACTC	CTCCAGAAAA	ACNGACAGGG	CAGGCTTGCA	TGAAAAGTN	ACATCTGCGT	420
TACAAAGTCT	ATCTTCCTCA	NANGTCTGTN	AAGGAACAAT	TTAATCTTCT	AGCTTT	476

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ACTCTTTCTA ATGCTGATAT GATCTTGAGT ATAAGAATGC ATATGTCACT AGAATGGATA

60

AAATAATGCT GCAAACCTAA TGTTCTTATG CAAAATGGAA CGCTAATGAA ACACAGCTTA	120
CAATCGCAAA TCAAAACTCA CAAGTGCCTA TCTGTTGTAG ATTTAGTGTA ATAAGACTTA	180
GATTGTGCTC CTTCGGATAT GATTGTTCT CANATCTTGG GCAATNTTCC TTAGTCAAAT	240
CAGGCTACTA GAATTCTGTT ATTGGATATN TGAGAGCATG AAATTTTAA NAATACACTT	300
GTGATTATNA AATTAATCAC AAATTCACT TATACCTGCT ATCAGCAGCT AGAAAAACAT	360
NTNNNTTTTA NATCAAAGTA TTTTGTGTTT GGAANTGTNN AAATGAAATC TGAATGTGGG	420
TTCNATCTTA TTTTTCCCN GACNACTANT TNCTTTTTA GGGNCTATTG TGANCCATC	479

## (2) INFORMATION FOR SEQ ID NO:98:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGTGACTTGT CCTCCAACAA AACCCCTTGA TCAAGTTGT GGCAC TGACA ATCAGACCTA	60
TGCTAGTTCC TGTCATCTAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA	120
TCAACTCCAG CTGGATTATT TTGGAGCCTG CAAATCTATT CCTACTTGTA CGGACTTTGA	180
AGTGATTCAAG TTTCTCTAC GGATGAGAGA CTGGCTCAAG AATATCCTCA TGCAGCTTTA	240
TGAAGCCACT CTGAACACGC TGGTTATCTA GATGAGAACAGAGAAATAAA GTCAGAAAAT	300
TTACCTGGAG AAAAGAGGCT TTGGCTGGGG ACCATCCCAT TGAACCTTCT CTTAAGGACT	360
TTAAGAAAAA CTACCACATG TTGTGTATCC TGGTGCCGGC CGTTTATGAA CTGACCACCC	420
TTTCCAATAA TCTTGACGCT CCTGAACATTG CCTCCTCTGCG A	461

## (2) INFORMATION FOR SEQ ID NO:99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGGCCGC CGCAGGTGTTT CCTCGTACCG CAGGGCCCCC TCCCTTCCCC AGGCGTCCCT	60
CGGCGCCTCT CGGGGCCCGA GGAGGAGCGG CTGGCGGGTG GGGGGAGTGT GACCCACCC	120
CGGTGAGAAA AGCCTTCTCT AGCGATCTGA GAGGCCTGCC TTGGGGGTAC C	171

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CGGCCGCAAG	TGCAACTCCA	GCTGGGGCCG	TGCGGACGAA	GATTCTGCCA	GCAGTTGGTC	60
CGACTGCGAC	GACGGCGGCG	GCGACAGTCG	CAGGTGCAGC	GCAGGGCGCCT	GGGGTCTTGC	120
AAGGCTGAGC	TGACGCCGCA	GAGGTCGTGT	CACGTCCAC	GACCTTGACG	CCGTCGGGGA	180
CAGCCGGAAC	AGAGCCCGGT	GAAGCGGGAG	GCCTCGGGGA	GCCCCTCGGG	AAGGGCGGCC	240
CGAGAGATAC	GCAGGTGCAG	GTGGCCGCC				269

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTTTTTTTT	TTTTGGAATC	TACTGCGAGC	ACAGCAGGTC	AGCAACAAGT	TTATTTGCA	60
GCTAGCAAGG	TAACAGGGTA	GGGCATGGTT	ACATGTTCA	GTCAACTTCC	TTTGTCTGG	120
TTGATTGGTT	TGTCTTATG	GGGGCGGGGT	GGGGTAGGGG	AAACGAAGCA	AATAACATGG	180
AGTGGGTGCA	CCCTCCCTGT	AGAACCTGGT	TACAAAGCTT	GGGGCAGTTC	ACCTGGTCTG	240
TGACCGTCAT	TTTCTTGACA	TCAATGTTAT	TAGAAGTCAG	GATATCTTT	AGAGAGTCCA	300
CTGTTCTGGA	GGGAGAGATTAG	GGTTTCTTGC	CAAATCCAAC	AAAATCCACT	GAAAAAGTTG	360
GATGATCAGT	ACGAATACCG	AGGCATATTC	TCATATCGGT	GGCCA		405

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
GGCACTTAAT	CCATTTTAT	TTCAAAATGT	CTACAAATT	AATCCCATT	TACGGTATT	120
TCAAAATCTA	AATTATTCAA	ATTAGCCAAA	TCCTTACCAA	ATAATACCC	AAAATCAAA	180
ATATACTTCT	TTCAGCAAAC	TTGTTACATA	AATTAAAAAA	ATATATACGG	CTGGTGTTT	240
CAAAGTACAA	TTATCTTAAC	ACTGCAAACA	TTTTAAGGAA	CTAAAATAAA	AAAAAACACT	300
CCGCAAAGGT	TAAAGGGAAC	AACAAATTCT	TTTACAACAC	CATTATAAAA	ATCATATCTC	360
AAATCTTAGG	GGAATATATA	CTTCACACGG	GATCTTAAC	TTTACTCACT	TTGTTTATT	420
TTTAAACCA	TTGTTGGGC	CCAACACAAT	GGAATCCCCC	CTGGACTAGT		470

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TTTTTTTTT TTTTTTTG A CCCCCCTCTT ATAAAAAAACA AGTTACCATT TTATTTACT	60
TACACATATT TATTATCAA TTGGTATTAG ATATTCAAAA GGCAGCTTT AAAATCAAAC	120
TAAATGGAAA CTGCCTTAGA TACATAATT C TTAGGAATTA GCTTAAAATC TGCCTAAAGT	180
GAAAATCTTC TCTAGCTCTT TTGACTGTAA ATTTTGACT CTTGTAAAAC ATCCAAATTC	240
ATTTTCTTG TCTTTAAAAT TATCTAATCT TTCCATTTT TCCCTATTCC AAGTCAATT	300
GCTTCTCTAG CCTCATTCC TAGCTCTTAT CTACTATTAG TAAGTGGCTT TTTTCCTAAA	360
AGGGAAAACA GGAAGAGAAA TGGCACACAA AACAAACATT TTATATTCAAT ATTCTACCT	420
ACGTTAATAA AATAGCATT TGTGAAGCCA GCTCAAAAGA AGGCTTAGAT CCTTTTATGT	480
CCATTTAGT CACTAACGA TATCAAAGTG CCAGAATGCA AAAGGTTGT GAACATTAT	540
TCAAAAGCTA ATATAAGATA TTTCACATAC TCATCTTCT G	581

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTTTTTTTT TTTTTCTCTT CTTTTTTTTT GAAATGAGGA TCGAGTTTT	60
CACTCTCTAG ATAGGGCATG AAGAAAATC ATCTTCCAG CTTTAAAATA ACAATCAAAT	120
CTCTTATGCT ATATCATATT TTAAGTTAAA CTAATGAGTC ACTGGCTTAT CTTCTCCTGA	180
AGGAAATCTG TTCATTCTTC TCATTCAAT AGTTATATCA AGTACTACCT TGCATATTGA	240
GAGGTTTTTC TTCTCTATT ACACATATAT TTCCATGTGA ATTTGTATCA AACCTTTATT	300
TTCATGCAA CTAGAAAATA ATGTTCTTT TGCATAAGAG AAGAGAACAA TATAGCATT	360
CAAAACTGCT CAAATTGTTT GTTAAGTTAT CCATTATAAT TAGTTGGCAG GAGCTAATAC	420
AAATCACATT TACGACAGCA ATAATAAAC TGAAGTACCA GTTAAATATC CAAAATAATT	480
AAAGGAACAT TTTAGCCTG GGTATAATTA GCTAATTAC TTTACAAGCA TTTATTAGAA	540
TGAATTACACA TGTTATTATT CCTAGCCAA CACAATGG	578

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TTTTTTTTT	TTTTCAGTA	ATAATCAGAA	CAATATTTAT	TTTTATATTT	AAAATTCATA	60
GAAAAGTGC	TTACATTAA	TAAAAGTTG	TTTCTCAAAG	TGATCAGAGG	AATTAGATAT	120
GTCTTGAAC	CCAATATTAA	TTTGAGGAAA	ATACACCAAA	ATACATTAAG	TAAATTATTT	180
AAGATCATAG	AGCTTGTAAG	TGAAAAGATA	AAATTTGACC	TCAGAAACTC	TGAGCATTAA	240
AAATCCACTA	TTAGCAAATA	AATTACTATG	GAECTCTTGC	TTTAATTTG	TGATGAATAT	300
GGGGTGTCA	C	TGGTAAACCA	ACACATTCTG	AAGGATACAT	TACTTAGTGA	360
TGTACTTTGC	TAATACGTGG	ATATGAGTTG	ACAAGTTCT	CTTCTTCAA	TCTTTAAGG	420
GGCGAGAAAT	GAGGAAGAAA	AGAAAAGGAT	TACGCATACT	GTTCTTCTA	TGGAAGGATT	480
AGATATGTTT	CCTTGCCAA	TATTAACAAA	ATAATAATGT	TTACTACTAG	TGAAACCC	538

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TTTTTTTTT	TTTTTAGTC	AAGTTTCTAT	TTTTATTATA	ATTAAAGTCT	TGGTCATTTC	60
ATTATTAGC	TCTGCAACTT	ACATATTAA	ATTAAAGAAA	CGTTTAGAC	AACTGTACAA	120
TTTATAAATG	TAAGGTGCCA	TTATTGAGTA	ATATATTCT	CCAAGAGTGG	ATGTGTCCCT	180
TCTCCCACCA	ACTAAATGAAC	AGCAACATTA	GTAAATTAA	ATTAGTAGAT	ATACACTGCT	240
GCAAACGCTA	ATTCTCTTCT	CCATCCCCAT	GTGATATTGT	GTATATGTGT	GAGTTGGTAG	300
AATGCATCAC	AATCTACAAT	CAACAGCAAG	ATGAAGCTAG	GCTGGGCTTT	CGGTGAAAAT	360
AGACTGTGTC	TGTCTGAATC	AAATGATCTG	ACCTATCCTC	GGTGGCAAGA	ACTCTTCGAA	420
CCGCTTCCTC	AAAGGCGCTG	CCACATTGT	GGCTCTTGC	ACTTGTTC	AAA	473

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CGCCATGGCA	CTGCAGGGCA	TCTCGGTCA	GGAGCTGTCC	GGCCTGGCCC	CGGGCCCGTT	60
CTGTGCTATG	GTCCTGGCTG	ACTTCGGGGC	GCGTGTGGTA	CGCGTGGACC	GGCCCGGCTC	120
CCGCTACGAC	GTGAGCCGCT	TGGGCCGGGG	CAAGCGCTCG	CTAGTGCTGG	ACCTGAAGCA	180
GCCGCGGGGA	GCCGCCGTGC	TGCGGCGTCT	GTGCAAGCGG	TCGGATGTGC	TGCTGGAGCC	240
CTTCCGCCGC	GGTGTCA	AGAAAACCTCA	GCTGGGCCA	GAGATTCTGC	AGCGGGAAAA	300
TCCAAGGCTT	ATTATGCCA	GGCTGAGTGG	ATTGGCCAG	TCAGGAAGCT	TCTGCCGGTT	360
AGCTGGCCAC	GATATCAACT	ATTGGCTTT	GTCAGGTGTT	CTCTCAAAAA	TTGGCAGAAG	420
TGGTGAGAAAT	CCGTATGCC	CGCTGAATCT	CCTGGCTGAC	TTGCTGGTG	GTGGCCTTAT	480
GTGTGCACTG	GGCATTATAA	TGGCTTTT	TGACCGCACA	CGCACTGACA	AGGGTCAGGT	540

CATTGATGCA AATATGGTGG AAGGAACAGC ATATTTAAGT TCTTTCTGT GGAAAACCTCA 600  
 GAAATCGAGT CTGTGGGAAG CACCTCGAGG ACAGAACATG TTGGATGGTG GAGCACCTT 660  
 CTATACGACT TACAGGACAG CAGATGGGA ATTCACTGGCT GTTGGAGCAA TAGAACCCCA 720  
 GTTCTACGAG CTGCTGATCA AAGGACTTGG ACTAAAGTCT GATGAACCTC CCAATCAGAT 780  
 GAGCATGGAT GATTGGCCAG AAATGAAGAA GAAGTTGCA GATGTATTTG CAAAGAAGAC 840  
 GAAGGCAGAG TGGTGTCAAA TCTTGACGG CACAGATGCC TGTGTGACTC CGGTTCTGAC 900  
 TTTTGAGGAG GTTGTTCATC ATGATCACAA CAAGGAACGG GGCTCGTTA TCACCAGTGA 960  
 GGAGCAGGAC GTGAGCCCCC GCCCTGCACC TCTGCTGTTA AACACCCAG CCATCCCTTC 1020  
 TTTCAAAAGG GATCCTTCA TAGGAGAACAA CACTGAGGAG ATACTTGAAG AATTTGGATT 1080  
 CAGCCGCGAA GAGATTATC AGCTTAACTC AGATAAAATC ATTGAAAGTA ATAAGGTAAA 1140  
 AGCTAGTCTC TAACTTCCAG GCCCACGGCT CAAGTGAATT TGAATACTGC ATTACAGTG 1200  
 TAGAGTAACA CATAACATTG TATGCATGGA AACATGGAGG AACAGTATTA CAGTGTCTA 1260  
 CCACTCTAAT CAAGAAAAGA ATTACAGACT CTGATTCTAC AGTGATGATT GAATTCTAAA 1320  
 AATGGTTATC ATTAGGGCTT TTGATTATA AAACTTGGG TACTTATACT AAATTATGGT 1380  
 AGTTATTCTG CCTTCCAGTT TGCTTGATAT ATTTGTTGAT ATTAAGATT TTGACTTATA 1440  
 TTTTGAATGG GTTCTAGTGA AAAAGGAATG ATATATTCTT GAAGACATCG ATATACATT 1500  
 ATTTACACTC TTGATTCTAC AATGTAGAAA ATGAGGAAAT GCCACAAATT GTATGGTGT 1560  
 AAAAGTCACG TGAAACAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 1620  
 A 1621

## (2) INFORMATION FOR SEQ ID NO:108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met	Ala	Leu	Gln	Gly	Ile	Ser	Val	Met	Glu	Leu	Ser	Gly	Leu	Ala	Pro
1								5		10				15	
Gly	Pro	Phe	Cys	Ala	Met	Val	Leu	Ala	Asp	Phe	Gly	Ala	Arg	Val	Val
								20		25			30		
Arg	Val	Asp	Arg	Pro	Gly	Ser	Arg	Tyr	Asp	Val	Ser	Arg	Leu	Gly	Arg
								35		40			45		
Gly	Lys	Arg	Ser	Leu	Val	Leu	Asp	Leu	Lys	Gln	Pro	Arg	Gly	Ala	Ala
								50		55			60		
Val	Leu	Arg	Arg	Leu	Cys	Lys	Arg	Ser	Asp	Val	Leu	Leu	Glu	Pro	Phe
								65		70			75		80
Arg	Arg	Gly	Val	Met	Glu	Lys	Leu	Gln					Ile	Leu	Gln
								85		90			95		
Arg	Glu	Asn	Pro	Arg	Leu	Ile	Tyr	Ala	Arg	Leu	Ser	Gly	Phe	Gly	Gln
								100		105			110		
Ser	Gly	Ser	Phe	Cys	Arg	Leu	Ala	Gly	His	Asp	Ile	Asn	Tyr	Leu	Ala
								115		120			125		
Leu	Ser	Gly	Val	Leu	Ser	Lys	Ile	Gly	Arg	Ser	Gly	Glu	Asn	Pro	Tyr
								130		135			140		
Ala	Pro	Leu	Asn	Leu	Leu	Ala	Asp	Phe	Ala	Gly	Gly	Gly	Leu	Met	Cys
								145		150			155		160
Ala	Leu	Gly	Ile	Ile	Met	Ala	Leu	Phe	Asp	Arg	Thr	Arg	Thr	Asp	Lys
								165		170			175		
Gly	Gln	Val	Ile	Asp	Ala	Asn	Met	Val	Glu	Gly	Thr	Ala	Tyr	Leu	Ser
								180		185			190		
Ser	Phe	Leu	Trp	Lys	Thr	Gln	Lys	Ser	Ser	Leu	Trp	Glu	Ala	Pro	Arg
								195		200			205		

Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg  
 210 215 220  
 Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe  
 225 230 235 240  
 Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro  
 245 250 255  
 Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala  
 260 265 270  
 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp  
 275 280 285  
 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val  
 290 295 300  
 His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu  
 305 310 315 320  
 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala  
 325 330 335  
 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu  
 340 345 350  
 Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn  
 355 360 365  
 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu  
 370 375 380

## (2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGCACGAGGC	TGCGCCAGGG	CCTGAGCGGA	GGCGGGGGCA	GCCTGCCAG	CGGGGGCCCC	60
GGGCCTGGCC	ATGCCTCACT	GAGCCAGCGC	CTGCGCCTCT	ACCTCGCCGA	CAGCTGGAAC	120
CAGTGCAGCC	TAGTGGCTCT	CACCTGCTTC	CTCCTGGCG	TGGGCTGCCG	GCTGACCCCG	180
GTGTTGTACC	ACCTGGGCCG	CACTGTCCTC	TGCATCGACT	TCATGGTTTT	CACGGTGCAG	240
CTGCTTCACA	TCTTCACGGT	CAACAAACAG	CTGGGGCCCA	AGATCGTCAT	CGTGAGCAAG	300
ATGATGAAGG	ACGTGTTCTT	CTTCCTCTTC	TTCCCTCGCG	TGTGGCTGGT	AGCCTATGGC	360
GTGGCCACCG	AGGGGCTCCT	GAGGCCACGG	GACAGTGACT	TCCCAAGTAT	CCTGCGCCGC	420
GTCTTCTACC	GTCCCTACCT	GCAGATCTTC	GGGCAGATTG	CCCAGGAGGA	CATGGACGTG	480
GCCCTCATGG	AGCACAGCAA	CTGCTCGTCG	GAGCCCGGCT	TCTGGGCACA	CCCTCCTGGG	540
GCCCAGGCCG	GCACCTCGGT	CTCCCCAGTAT	GCCAAGTGGC	TGGTGGTGCT	GCTCCTCGTC	600
ATCTTCCTGC	TCGTGGCCAA	CATCCTGCTG	GTCAAATTGTC	TCATTGCCAT	GTTCAGTTAC	660
ACATTGGCA	AAGTACAGGG	CAACAGCGAT	CTCTACTGGG	AGGCGCAGCG	TTACCGCCTC	720
ATCCGGGAAT	TCCACTCTCG	GCCCCGCGCTG	GCCCCGCCCT	TTATCGTCAT	CTCCCACCTTG	780
CGCCTCCTGC	TCAGGCAATT	GTGCAGGCCA	CCCCGGAGCC	CCCAGCCGTC	CTCCCCGGCC	840
CTCGAGCATT	TCCGGGTTTA	CCTTTCTAAG	GAAGCCGAGC	GGAAAGCTGCT	AACGTGGAA	900
TCGGTGCATA	AGGAGAACCTT	TCTGCTGGCA	CGCGCTAGGG	ACAAGCGGGA	GAGCGACTCC	960
GAGCGTCTGA	AGCGCACGTC	CCAGAACGGTG	GACTTGGCAC	TGAAACAGCT	GGGACACATC	1020
CGCGAGTACG	AACAGCGCCT	GAAAGTGTG	GAGCGGGAGG	TCCAGCAGTG	TAGCCCGTGC	1080
CTGGGGTGGG	TGGCCGAGGC	CCTGAGCCGC	TCTGCGCTTG	TGCCCCCAGG	TGGGCCGCCA	1140
CCCCCTGACC	TGCCTGGGTC	CAAAGACTGA	GCCCTGCTGG	CGGACTTCAA	GGAGAACGCC	1200
CCACAGGGGA	TTTGCTCCT	AGAGTAAGGC	TCATCTGGGC	CTCGGCCCCC	GCACCTGGTG	1260
GCCTTGTCT	TGAGGTGAGC	CCCATGTCCA	TCTGGGCCAC	TGTCAGGACC	ACCTTTGGGA	1320
GTGTCATCCT	TACAAACCAC	AGCATGCCCG	GCTCCTCCCA	GAACCAGTCC	CAGCCTGGGA	1380

GGATCAAGGC	CTGGATCCCG	GGCCGTTATC	CATCTGGAGG	CTGCAGGGTC	CTTGGGGTAA	1440
CAGGGACAC	AGACCCCTCA	CCACTCACAG	ATTCTCACA	CTGGGGAAAT	AAAGCCATT	1500
CAGAGGAAAA	AAAAAAAAAA	AAAA				1524

## (2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGGAACCAGC	CTGCACGCGC	TGGCTCCGGG	TGACAGCCGC	GCGCCTCGGC	CAGGATCTGA	60
GTGATGAGAC	GTGTCCCCAC	TGAGGTGCC	CACAGCAGCA	CGTGGTGAGC	ATGGGCTGAG	120
AAGCTGGACC	GGCACCAAAG	GGCTGGCAGA	AATGGGCGCC	TGGCTGATT	CTAGGCAGTT	180
GGCGGCAGCA	AGGAGGAGAG	GCCGAGCTT	CTGGAGCAGA	GCCGAGACGA	AGCAGTTCTG	240
GAGTGCCTGA	ACGGCCCCCT	GAGCCCTACC	CGCCTGGCCC	ACTATGGTCC	AGAGGCTGTG	300
GGTGAGCCGC	CTGCTGCGC	ACCGGAAAGC	CCAGCTCTTG	CTGGTCAACC	TGCTAACCTT	360
TGGCCTGGAG	GTGTGTTGG	CCGCAGGCAT	CACCTATGTG	CCGCCTCTGC	TGCTGGAAGT	420
GGGGTAGAG	GAGAAGTTCA	TGACCATGGT	GCTGGGCATT	GGTCCAGTGC	TGGCCTGGT	480
CTGTGTCCCG	CTCCTAGGCT	CAGCCAGTGA	CCACTGGCGT	GGACGCTATG	GCCGCCGCCG	540
GCCCTTCATC	TGGGCACTGT	CCTTGGGCAT	CCTGCTGAGC	CTCTTCTCA	TCCCAAGGGC	600
CGGCTGGCTA	GCAGGGCTGC	TGTGCCCGGA	TCCCAGGCC	CTGGAGCTGG	CACTGCTCAT	660
CCTGGCGTG	GGGCTGCTGG	ACTTCTGTGG	CCAGGTGTGC	TTCACTCCAC	TGGAGGCCCT	720
GCTCTCTGAC	CTCTTCCGGG	ACCCGGACCA	CTGTCGCCAG	GCCTACTCTG	TCTATGCCCT	780
CATGATCAGT	CTTGGGGGCT	GCCTGGCTA	CCTCCTGCCT	GCCATTGACT	GGGACACCAAG	840
TGCCCTGGCC	CCCTACCTGG	GCACCCAGGA	GGAGTGCCTC	TTTGGCCTGC	TCACCCCTCAT	900
CTTCCTCACC	TGCGTAGCAG	CCACACTGCT	GGTGGCTGAG	GAGGCAGCGC	TGGGCCAAC	960
CGAGCCAGCA	GAAGGGCTGT	CGGCCCCCTC	CTTGTGCC	CACTGCTGTC	CATGCCGGGC	1020
CCGCTTGGCT	TTCCGGAACC	TGGGCGCCCT	GCTTCCCCGG	CTGCACCAGC	TGTGCTGCCG	1080
CATGCCCGC	ACCCCTGCGCC	GGCTCTCGT	GGCTGAGCTG	TGAGCTGGA	TGGCACTCAT	1140
GACCTTCACG	CTGTTTACA	CGGATTTCGT	GGGCGAGGGG	CTGTACCAAGG	GGGTGCCCAG	1200
AGCTGAGCCG	GGCACCGAGG	CCCGGAGACA	CTATGATGAA	GGCCTTCGGA	TGGGAGCCT	1260
GGGGCTGTT	CTGCAGTGC	CCATCTCCCT	GGTCTTCTCT	CTGGTCATGG	ACCGGCTGGT	1320
GCAGCGATT	GGCACCTCGAG	CAGTCTATT	GGCCAGTGTG	GCAGCTTCC	CTGTGGCTGC	1380
CGGTGCCACA	TGCCTGTCCC	ACAGTGTGGC	CGTGGTGACA	GCTTCAGCCG	CCCTCACCGG	1440
GTTCACCTTC	TCAGCCCTGC	AGATCCTGCC	CTACACACTG	GCCTCCCTCT	ACCAACGGGA	1500
GAAGCAGGTG	TTCCTGCCA	AATACCGAGG	GGACACTGGA	GGTGTAGCA	GTGAGGACAG	1560
CCTGATGACC	AGCTTCCCTGC	CAGGCCCTAA	GCCTGGAGCT	CCCTCCCTA	ATGGACACGT	1620
GGGTGCTGGA	GGCAGTGGCC	TGCTCCCACC	TCCACCCGCG	CTCTGCGGGG	CCTCTGCC	1680
TGATGTCTCC	GTACGTGTGG	TGGTGGGTGA	GCCCACCGAG	GCCAGGGTGG	TTCCGGGCCG	1740
GGGCATCTGC	CTGGACCTCG	CCATCCTGGA	TAGTGCCTC	CTGCTGTCCC	AGGTGGCC	1800
ATCCCTGTTT	ATGGGCTCCA	TTGTCCAGCT	CAGCCAGTCT	GTCACTGCCT	ATATGGTGT	1860
TGCCGCAGGC	CTGGGTCTGG	TCGCCATT	CTTGCTACA	CAGGTAGTAT	TTGACAAGAG	1920
CGACTTGGCC	AAATACTCAG	CGTAGAAAAC	TTCCAGCACA	TTGGGGTGG	GGGCCTGCCT	1980
CACTGGGTCC	CAGCTCCCCG	CTCCTGTTAG	CCCCATGGGG	CTGCCGGGCT	GGCCGCCAGT	2040
TTCTGTTGCT	GCCAAAGTAA	TGTGGCTCTC	TGCTGCCACC	CTGTGCTGCT	GAGGTGCGTA	2100
GCTGCACAGC	TGGGGCTGG	GGCGTCCCTC	TCCTCTCTCC	CCAGTCTCTA	GGGCTGCCTG	2160
ACTGGAGGCC	TTCCAAGGGG	GTTCAGTCT	GGACTTATAC	AGGGAGGCCA	GAAGGGCTCC	2220
ATGCACTGGA	ATGCCGGGAC	TCTGCAGGTG	GATTACCCAG	GCTCAGGGTT	AACAGCTAGC	2280
CTCCTAGTTG	AGACACACCT	AGAGAAGGGT	TTTTGGGAGC	TGAATAACT	CAGTCACCTG	2340
GTTTCCCATC	TCTAACCTGCA	GCTTCGTTA	ATGTAGCTCT	TGCATGGGAG	2400	
TTTCTAGGAT	GAAACACTCC	TCCATGGGAT	TTGAACATAT	GACTTATTG	TAGGGGAAGA	2460
GTCCTGAGGG	GCAACACACA	AGAACACAGGT	CCCCTCAGCC	CACAGCACTG	TCTTTTGCT	2520

GATCCACCCC CCTCTTACCT TTTATCAGGA TGTGGCCTGT TGGCCTTCT GTGCCATCA	2580
CAGAGACACA GGCATTTAAA TATTAACTT ATTTATTTAA CAAAGTAGAA GGGATCCAT	2640
TGCTAGCTTT TCTGTGTTGG TGTCTAATAT TTGGGTAGGG TGGGGATCC CCAACAATCA	2700
GGTCCCTGA GATAGCTGGT CATTGGGCTG ATCATTGCCA GAATCTTCTT CTCCCTGGGT	2760
CTGGCCCCCC AAAATGCCTA ACCCAGGACC TTGGAAATTCTACTCATCCC AAATGATAAT	2820
TCCAAATGCT GTTACCCAAG GTTACGGGTGT TGAAGGAAGG TAGAGGGTGG GGCTTCAGGT	2880
CTCAACGGCT TCCCTAACCA CCCCTCTTCT CTTGGCCAG CCTGGTCCC CCCACTTCCA	2940
CTCCCCTCTA CTCTCTCTAG GACTGGGCTG ATGAAGGCAC TGCCCAAAT TTCCCCTTACC	3000
CCCAACTTTC CCCTACCCCC AACTTCCCC ACCAGCTCCA CAACCCTGTT TGGAGCTACT	3060
GCAGGACCAG AAGCACAAAG TGCGGTTCC CAAGCCTTG TCCATCTCAG CCCCCAGAGT	3120
ATATCTGTGC TTGGGAATC TCACACAGAA ACTCAGGAGC ACCCCCTGCC TGAGCTAAGG	3180
GAGGTCTTAT CTCTCAGGGG GGGTTAAAGT GCCGTTGCA ATAATGTCGT CTTATTATT	3240
TAGCGGGGTG AATATTTAT ACTGTAAGTG AGCAATCAGA GTATAATGTT TATGGTGACA	3300
AAATTAAAGG CTTTCTTATA TGTTAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA	3360
AAAAAAAARA AAAAAAAA AAAAAAATAA AAAAAAAA	3410

## (2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCCAGGCGT CCCTCTGCCT GCCCACTCAG TGGCAACACC CGGGAGCTGT TTTGTCTTT	60
GTGGAGCCTC AGCAGTTCCC TCTTTCAGAA CTCACTGCCA AGAGCCCTGA ACAGGAGCCA	120
CCATGCAGTG CTTCAGCTTC ATTAAGACCA TGATGATCCT CTTCAATTG CTCATCTTTC	180
TGTGTGGTGC AGCCCTGTTG GCAGTGGGCA TCTGGGTGTC AATCGATGGG GCATCCTTTC	240
TGAAGATCTT CGGGCCACTG TCGTCCAGTG CCATGCAGTT TGTCAACGTG GGCTACTTCC	300
TCATCCGAGC CGGCGTTGTG GTCTTGCTC TTGGTTCTC GGGCTGCTAT GGTGCTAAGA	360
CTGAGAGCAA GTGTGCCCTC GTGACGTTCT TCTTCATCCT CCTCCTCATC TTCATTGCTG	420
AGGTTGCAGC TGCTGTGGTC GCCTTGGTGT ACACCACAAT GGCTGAGCAC TTCCTGACGT	480
TGCTGGTAGT GCCTGCCATC AAGAAAGATT ATGGTTCCCA GGAAGACTTC ACTCAAGTGT	540
GGAACACACC CATGAAAGGG CTCAAGTGCT GTGGCTTCAC CAACTATACG GATTTGAGG	600
ACTCACCCCTA CTTCAAAGAG AACAGTGCCT TTCCCCCATT CTGTTGCAAT GACAACGTCA	660
CCAACACAGC CAATGAAACC TGCACCAAGC AAAAGGCTCA CGACCAAAAA GTAGAGGGTT	720
GCTTCAATCA GCTTTGTAT GACATCCGAA CTAATGCAGT CACCGTGGGT GGTGTGGCAG	780
CTGGAATTGG GGGCCTCGAG CTGGCTGCCA TGATTGTGTC CATGTATCTG TACTGCAATC	840
TACAATAAGT CCACTTCTGC CTCTGCCACT ACTGCTGCCA CATGGGAACT GTGAAGAGGC	900
ACCCTGGCAA GCAGCAGTGA TTGGGGGAGG GGACAGGATC TAACAATGTC ACTTGGGCCA	960
GAATGGACCT GCCCTTCTG CTCCAGACTT GGGGCTAGAT AGGGACCACT CCTTTAGCG	1020
ATGCCTGACT TTCTTCCAT TGGTGGGTGG ATGGGTGGGG GGCATTCCAG AGCCTCTAAG	1080
GTAGCCAGTT CTGTTGCCA TTCCCCCAGT CTATTAAACC CTTGATATGC CCCCTAGGCC	1140
TAGTGGTGAT CCCAGTGCTC TACTGGGGGA TGAGAGAAAG GCATTTATA GCCTGGGCAT	1200
AAGTGAATC AGCAGAGCCT CTGGGTGGAT GTGTAGAAGG CACTTCAAAA TGCATAAACCC	1260
TGTTACAATG TAAAAAAA AAAAAAAA	1289

## (2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln  
 5 10 15  
 1  
 Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe  
 20 25 30  
 Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala  
 35 40 45  
 Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu  
 50 55 60  
 Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro  
 65 70 75 80  
 Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser  
 85 90 95  
 Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys  
 100 105 110  
 Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe  
 115 120 125  
 Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe  
 130 135 140  
 Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys  
 145 150 155 160  
 Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu  
 165 170 175  
 Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Arg Gln  
 180 185 190  
 Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu  
 195 200 205  
 His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr  
 210 215 220  
 Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp  
 225 230 235 240  
 Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val  
 245 250 255  
 Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg  
 260 265 270  
 Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly  
 275 280 285

Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly  
 290 295 300  
 Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 553 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala  
 1 5 10 15  
 Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu  
 20 25 30  
 Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Glu Val Gly Val  
 35 40 45  
 Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly  
 50 55 60  
 Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly  
 65 70 75 80  
 Arg Tyr Gly Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile  
 85 90 95  
 Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu  
 100 105 110  
 Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly  
 115 120 125  
 Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu  
 130 135 140  
 Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala  
 145 150 155 160  
 Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr  
 165 170 175  
 Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu  
 180 185 190  
 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu  
 195 200 205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly  
210 215 220

Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His  
225 230 235 240

Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu  
245 250 255

Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg  
260 265 270

Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe  
275 280 285

Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val  
290 295 300

Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
305 310 315 320

Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
325 330 335

Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
340 345 350

Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
355 360 365

Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
370 375 380

Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
385 390 395 400

Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
405 410 415

Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
420 425 430

Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
435 440 445

Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser  
450 455 460

Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala  
465 470 475 480

Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
485 490 495

Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
500 505 510

Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
515 520 525

Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp

530

535

540

Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
 545 550

## (2) INFORMATION FOR SEQ ID NO:114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu  
 1 5 10 15

Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val  
 20 25 30

Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser  
 35 40 45

Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly  
 50 55 60

Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr  
 65 70 75 80

Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Ile Leu Leu Ile  
 85 90 95

Phe Ile Ala Glu Val Ala Ala Val Val Ala Leu Val Tyr Thr Thr  
 100 105 110

Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys  
 115 120 125

Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met  
 130 135 140

Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp  
 145 150 155 160

Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn  
 165 170 175

Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala  
 180 185 190

His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile  
 195 200 205

Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly  
 210 215 220

Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu  
 230  
 225  
 235  
 240

Gln

## (2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 366 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo Sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCTTTCTC TCCCTCCTC TGAATTAAT TCTTCACT TGCATTGC AAGGATTACA  
 CATTCACTG TGATGTATAT TGTGTTCAA AAAAAAAA GTGTCTTG TTAAATTAC  
 TTGGTTGTG AATCCATCTT GCTTTTCCC CATTGAACT AGTCATTAAC CCATCTGA  
 ACTGGTAGAA AAACATCTGA AGAGCTAGTC TATCAGCATC TGACAGGTGA ATTGGATGGT  
 TCTCAGAACC ATTTCACCCA GACAGCTGT TTCTATCCTG TTAATAAAAT TAGTTGGGT  
 TCTCTACATG CATAACAAAC CCTGCTCAA TCTGTCACAT AAAAGTCGT GACTTGAAGT  
 TTAGTC

60  
 120  
 180  
 240  
 300  
 360  
 366

## (2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 282 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ACAAAGATGA ACCATTCT ATATTATAGC AAAATTAAA TCTACCCGT A TTCAATATT  
 GAGAAATGAG ATNAAACACA ATNTTATAA GTCTACTTAG AGAAGATCAA GTGACCTCAA  
 AGACTTACT ATTTCTAT TTTAAGACAC ATGATTATC CTATTTAGT AACCTGGTCA  
 ATACGTTAAA CAAAGGATAA TGTGAACAGC AGAGAGGATT TGTTGGCAGA AAATCTATGT  
 TCAATCTNGA ACTATCTANA TCACAGACAT TTCTATTCC TT

60  
 120  
 180  
 240  
 282

## (2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ACACATGTCG CTCACAGCCTCTAGATG CTTCTGGTCA ACATANAGGA ACAGGGACCA  
 TATTTATCCT CCCTCCTGAA ACAATTGCAA AATAANACAA AATATATGAA ACAATTGCAA  
 AATAAGGCAA AATATATGAA ACAACAGGTC TCGAGATATT GGAAATCAGT CAATGAAGGA  
 TACTGATCCC TGATCACTGT CCTAATGCAG GATGTGGAA ACAGATGAGG TCACCTCTGT  
 GACTGCCCA GCTTACTGCC TGTAGAGAGT TTCTANGCTG CAGTCAGAC AGGGAGAAAT

60  
120  
180  
240  
300  
305

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 71 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ACCAAGGTGT NTGAATCTCT GACGTGGGAA TCTCTGATTC CCGCACAAATC TGAGTGGAAA  
 AANTCCTGGG T

60  
71

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACACCA  
 GAAAATGGGG TGAAATTGGC CAACTTCTA TNAACTTATG TTGCAANTT TGCCACCAAC  
 AGTAAGCTGG CCCTTCTAAT AAAAGAAAAT TGAAAGGTT CTCACTAANC GGAATTAANT  
 AATGGANTCA AGANACTCCC AGGCCTCAGC GT

60  
120  
180  
212

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 90 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ACTCGTTGCA NATCAGGGC CCCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGCC	60
CTCCGCCGGC GCAGAACATG CTGGGGTGGT	90

## (2) INFORMATION FOR SEQ ID NO:121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGTANCAGTGA ANACGACAGA NAGGGTTGTC AAAAATGGAG AANCCTTGAA GTCATTTGA	60
GAATAAGATT TGCTAAAAGA TTTGGGGCTA AAACATGGTT ATTGGGAGAC ATTTCTGAAG	120
ATATNCANGT AAATTANGGA ATGAATTCTAT GGTTCTTTG GGAATTCCCTT TACGATNGCC	180
AGCATANACT TCATGTGGGG ATANCAGCTA CCCTTGTA	218

## (2) INFORMATION FOR SEQ ID NO:122:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG	60
CATTTGTTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT	120
CACCACCCCG GCGGGGTCTAT CTGTGCCACA GGTCCCTGTT GACAGTGCAGG T	171

## (2) INFORMATION FOR SEQ ID NO:123:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGTAGCGTGA AGACNACAGA ATGGTGTGTG CTGTGCTATC CAGGAACACA TTTATTATCA	60
TTATCAANTA TTGTGT	76

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ACCTTCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT	60
CAATGTGCTG GGTCAATATGG AGGGGAGGGAG ACTCTAAAAT AGCCAATTT ATTCTCTTGG	120
TTAAGATTTG T	131

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTGC GTTACCAACT ATACCACTGG	60
CTTGAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGACT TTTGCTCAGA TGCTGAAGAA	120
CTACAGTCTG CATTGGCAG AAATGAAGAT GAATTTGGAT TAAATGAGGA TGCTGAAGAT	180
TTGCCTCACC AAACAAAAGT GAAACAACGT AGAGAAAATT TTCAGGAAA AAGACAGTGG	240
CTCTTGAAGT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC	300
CATGGTGGGG GTCTTGCATC TGTAAGAATG GAATTGATT TGCTTTGCA AGAATCTCAG	360
CAGGAAACAT CAGAACCACT ATTTCTAGC CCTCTGTCAG AGCAACCTC AGTGCCTCTC	420
CTCTTGCTT GT	432

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACACAACTTG AATAGTAAAA TAGAAACTGA GCTGAAATT CTAATTCACT TTCTAACCAT 60  
 AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATTT ATAAAAAATTT GT 112

## (2) INFORMATION FOR SEQ ID NO:127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACCACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAC 54

## (2) INFORMATION FOR SEQ ID NO:128:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ACCTCATTAG TAATTGTTTT GTTGTTCAT TTTTTCTAA TGTCTCCCT CTACCAGCTC 60  
 ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTGC TCTCTGCTCA 120  
 TTCTCTCTGA AGTCTAGGTT ACCCATTG GGGACCCATT ATAGGCAATA AACACAGTTC 180  
 CCAAAGCATT TGGACAGTTT CTTGTTGTGT TTTAGAATGG TTTTCCTTT TCTTAGCCTT 240  
 TTCCTGCAAA AGGCTCACTC AGTCCCTTGC TTGCTCAGTG GACTGGGCTC CCCAGGGCCT 300  
 AGGCTGCCTT CTTTCCATG TCC 323

## (2) INFORMATION FOR SEQ ID NO:129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ACATACATGT GTGTATATTT TTAAATATCA CTTTGTATC ACTCTGACTT TTTAGCATAC 60  
 TGAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTCACTC 120

TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTTCAT TTCCCTTCACG TTGGCCAATG	180
GATAAAACAAA GT	192

## (2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 362 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCCTTTTTA TGGAATGAGT AGACTGTATG TTTGAANATT TANCCACAAC CTCTTGACA	60
TATAATGACG CAACAAAAAG GTGCTGTTA GTCCTATGGT TCAGTTATG CCCCTGACAA	120
GTTCCTCATTG TGTTTGGCG ATCTTCTGGC TAATCGTGGT ATCCTCCATG TTATTAGTAA	180
TTCTGTATTC CATTGGTTA ACGCCTGGTA GATGTAACCT GCTANGAGGC TAACTTTATA	240
CTTATTTAAA AGCTCTTATT TTGTGGTCAT TAAAATGGCA ATTATGTGC AGCACTTTAT	300
TGCAGCAGGA AGCACGTGTG GGTTGGTTGT AAAGCTCTT GCTAATCTTA AAAAGTAATG	360
GG	362

## (2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 332 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTTTTGAAA GATCGTGTCC ACTCCTGTGG ACATCTTGTGTT TTAATGGAGT TTCCCATGCA	60
GTANGACTGG TATGGTTGCA GCTGTCCAGA TAAAAACATT TGAAGAGCTC CAAAATGAGA	120
GTTCCTCCAG GTTCGCCCTG CTGCTCCAAG TCTCAGCAGC AGCCTCTTT AGGAGGCATC	180
TTCTGAACTA GATTAAGGCA GCTTGAAAT CTGATGTGAT TTGGTTTATT ATCCAACCAA	240
CTTCCATCTG TTATCACTGG AGAAAGCCCA GACTCCCCAN GACNGGTACG GATTGTGGC	300
ATANAAGGAT TGGGTGAAGC TGGCGTTGTG GT	332

## (2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 322 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

ACTTTGCCA	TTTGTTATAT	ATAAACAAATC	TTGGGACATT	CTCCTGAAAA	CTAGGTGTCC	60
AGTGGCTAAG	AGAACTCGAT	TTCAAGCAAT	TCTGAAAGGA	AAACCAGCAT	GACACAGAAAT	120
CTCAAATTCC	CAAACAGGGG	CTCTGTGGGA	AAAATGAGGG	AGGACCTTG	TATCTCGGGT	180
TTTAGCAAGT	TAAAATGAAN	ATGACAGGAA	AGGCTTATT	ATCAACAAAG	AGAAGAGTTG	240
GGATGCTTCT	AAAAAAAAC	TTGGTAGAGA	AAATAGGAAT	GCTNAATCCT	AGGGAAGCCT	300
GTAACAATCT	ACAATTGGTC	CA				322

## (2) INFORMATION FOR SEQ ID NO:133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ACAAGCCTTC	ACAAGTTAA	CTAAATTGGG	ATTAATCTTT	CTGTANTTAT	CTGCATAATT	60
CTTGTTCCTTC	TTTCCATCTG	GCTCCTGGGT	TGACAATTG	TGAAACAAAC	TCTATTGCTA	120
CTATTTAAAAA	AAAATCACAA	ATCTTCCCT	TTAAGCTATG	TTNAATTCAA	ACTATTCCCTG	180
CTATTCCCTGT	TTTGTCAAAG	AAATTATATT	TTTCAAAATA	TGTNTATTG	TTTGATGGGT	240
CCCACGAAAC	ACTAATAAAA	ACCACAGAGA	CCAGCCTG			278

## (2) INFORMATION FOR SEQ ID NO:134:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GTTTANAAAAA	CTTGTTCAGC	TCCATAGAGG	AAAGAATGTT	AAACTTTGTA	TTTTAAAACA	60
TGATTCTCTG	AGGTTAAACT	TGGTTTCAA	ATGTTATT	TACTTGTATT	TTGCTTTGG	120
T						121

## (2) INFORMATION FOR SEQ ID NO:135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACTTANAACC ATGCCTAGCA CATCAGAAC	60
ATANCAAGTG GTGACTGGTT AAGCGTGCAG CAAAGGTCA	120
AAACTTGATA CTTTTGTTCT AAGTAGGAAC TAGTATACAG TNCCTAGGAN	180
GGGTGCCCGG CAACTCCTGC AGCCGCTCCT CTGTGCCAGN	240
CCACCTCAAT CAAGCCCTGG GCCATGCTAC CTGCAATTGG	300
TTCCCAAGGA TGCAAAGCCT GGTGCTAAC	350
TCCTGGGGCG TCAACTCAGT	

## (2) INFORMATION FOR SEQ ID NO:136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

TGTACCGTGA AGACGACAGA AGTTGCATGG CAGGGACAGG GCAGGGCCGA GGCCAGGGTT	60
GCTGTGATTG TATCCGAATA NTCCTCGTGA GAAAAGATAA TGAGATGACG TGAGCAGCCT	120
GCAGACTTGT GTCTGCCTTC AANAAGCCAG ACAGGAAGGC CCTGCCTGCC TTGGCTCTGA	180
CCTGGCGGCC AGCCAGCCAG CCACAGGTGG GCTTCTTCCT TTTGTGGTGA CAACNCCAAG	240
AAAAGTGCAG AGGCCCAGGG TCAGGTGTNA GTGGGTANGT GACCATAAAA CACCAGGTGC	300
TCCCAGGAAC CCGGGCAAAG GCCATCCCCA CCTACAGCCA GCATGCCAC TGGCGTGATG	360
GGTGCAGANG GATGAAGCAG CCAGNTGTTG TGCTGTGGT	399

## (2) INFORMATION FOR SEQ ID NO:137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACTGGTGTGG TNGGGGGTGA TGCTGGTGGT ANAAGTTGAN GTGACTTCAN GATGGTGTGT	60
GGAGGAAGTG TGTGAACGTA GGGATGTAGA NGTTTGCGGC GTGCTAAATG AGCTTCGGGA	120
TTGGCTGGTC CCACTGGTGG TCACTGTCA	165
TGGTGGGGTT CCTGT	

## (2) INFORMATION FOR SEQ ID NO:138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ACTCACTGGA ATGCCACATT CACAACAGAA TCAGAGGTCT GTGAAAACAT TAATGGCTCC	60
TTAACTTCTC CAGTAAGAAT CAGGGACTTG AAATGGAAAC GTTAACAGCC ACATGCCCAA	120
TGCTGGCAG TCTCCCATGC CTTCCACAGT GAAAGGGCTT GAGAAAAATC ACATCCAATG	180
TCATGTGTTT CCAGCCACAC CAAAAGGTGC TTGGGGTGGA GGGCTGGGG CATANANGT	240
CANGCCTCAG GAAGCCTCAA GTTCCATTCA GCTTTGCCAC TGTACATTCC CCATNTTTAA	300
AAAAACTGAT GCCTTTTTT TTTTTTTTG TAAAATTTC	338

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGAATCTTG GTTTTGGCA TCTGGTTGC CTATAGCCGA GGCCACTTTG ACAGAACAAA	60
GAAAGGGACT TCGAGTAAGA AGGTGATTAA CAGCCAGCCT AGTGCCCGAA GTGAAGGAGA	120
ATTCAAACAG ACCTCGTCAT TCCTGGTGTG AGCCTGGTGTG GCTCACCGCC TATCATCTGC	180
ATTTGCCTTA CTCAGGTGCT ACCGGACTCT GGCCCCGTGAT GTCTGTAGTT TCACAGGATG	240
CCTTATTTGT CTTCTACACC CCACAGGGCC CCCTACTTCT TCGGATGTGT TTTAATAAT	300
GTCAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG	360
GCCTGGAACT TGTAAAGT GT	382

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAANCTT CTTTCTGTTG TGTTNGATTT TACTATAGGG GTTTNGCTTN TTCTAAANAT	60
ACTTTTCATT TAACANCTTT TGTAAAGTGT CAGGCTGCAC TTTGCTCCAT ANAATTATTG	120
TTTCACATT TCAAACGTGA TGTGTTGTC TCTTANAGCA TTGGTGAAAT CACATATTTC	180
ATATTCAGCA TAAAGGAGAA	200

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ACTTTATTTT CAAAACACTC ATATGTTGCA AAAAACACAT AGAAAAATAA AGTTGGTGG	60
GGGTGCTGAC TAAACTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGGTTTGT	120
ATGCATGTAG AGAACCCAAA CTAATTATT AAACAGGATA GAAACAGGCT GTCTGGGTGA	180
AATGGTTCTG AGAACCATCC AATTACCTG TCAGATGCTG ATANACTAGC TCTTCAGATG	240
TTTTCTTAC AGTCAGAGA TNGGTTAATG ACTANTCCA ATGGGGAAAA AGCAAGATGG	300
ATTCACAAAC CAAGTAATT TAAACAAAGA CACTT	335

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 459 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ACCAGGTTAA TATTGCCACA TATATCCTTT CCAATTGCGG GCTAACAGA CGTGTATTTA	60
GGGTTGTTTA AAGACAAACCC AGCTTAATAT CAAGAGAAAT TGTGACCTTT CATGGAGTAT	120
CTGATGGAGA AAACACTGAG TTTGACAAA TCTTATTTA TTCAGATAGC AGTCTGATCA	180
CACATGGTCC ACAAACACTC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATTGGTC	240
TTCAAACATC ATAGCCAATG ATGCCCGCT TGCCTATAAT CTCCTCGACA TAAAACCACA	300
TCAACACCTC AGTGGCCACC AAACCATTCA GCACAGCTTC CTTAACTGTG AGCTGTTGA	360
AGCTACCACT AGTGGCCACC AAACCATTCA GCACAGCTTC CTTAACTGTG AGCTGTTGA	420
CAGCANGGAGT GGGAGGAACC AGCTAACCT TGGCGTANT	459

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

ACATTTCTT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG	60
AAATCCAAAC AGTCTCTCCT AGAAAGGAAT AGTGTACCA ACCCCACCCA TCTCCCTGAG	120
ACCATCCGAC TTCCCTGTGT	140

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACTTCAGTAA CAACATACAA TAACAACATT AAGTGTATAT TGCCATCTT GTCATTTCT	60
ATCTATACCA CTCTCCCTTC TGAAAACAAN AATCACTANC CAATCACTTA TACAAATTTG	120
AGGCAATTAA TCCATATTTG TTTTCAATAA GGAAAAAAAG ATGT	164

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ACGTAGACCA TCCAACTTG TATTTGTAAT GGCAAACATC CAGNAGCAAT TCCTAAACAA	60
ACTGGAGGGT ATTTATACCC AATTATCCA TTCATTAACA TGCCCTCCTC CTCAGGCTAT	120
GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTGT ATAAACTTCA	180
GTAGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGAG GAAATGGAAC ATAAGCCCAG	240
TAGTAAAATN TTGCTTAGCT GAAACAGCCA CAAAGACTT ACCGCCGTGG TGATTACCAT	300
CAA	303

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ACTGCAGCTC AATTAGAAGT GGTCTCTGAC TTTCATCANC TTCTCCCTGG GCTCCATGAC	60
ACTGGCCTGG AGTGACTCAT TGCTCTGGTT GGTTGAGAGA GCTCCTTGC CAACAGGCCT	120
CCAAGTCAGG GCTGGGATTG GTTCCCTTTC CACATTCTAG CAACAATATG CTGGCCACTT	180
CCTGAACAGG GAGGGTGGGA GGAGCCAGCA TGGAACAAGC TGCCACTTTC TAAAGTAGCC	240
AGACTTGCCC CTGGGCTGT CACACCTACT GATGACCTTC TGTGCCTGCA GGATGGAATG	300
TAGGGGTGAG CTGTGTGACT CTATGGT	327

## (2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACATTGTTT TTTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTT	173

## (2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACAACCACCT TATCTCATCG AATTTTTAAC CCAAACCTCAC TCACTGTGCC TTTCTATCCT	60
ATGGGATATA TTATTTGATG CTCCATTCA TCACACATAT ATGAATAATA CACTCATACT	120
GCCCTACTAC CTGCTGCAAT AACACATTC CCTTCCTGTC CTGACCCCTGA AGCCATTGGG	180
GTGGTCCTAG TGGCCATCAG TCCANGCTG CACCTTGAGC CCTTGAGCTC CATTGCTCAC	240
NCCANCCCAC CTCACCGACC CCATCCTCTT ACACAGCTAC CTCCTTGCTC TCTAACCCCA	300
TAGATTATNT CCAAATTCAAG TCAATTAAAGT TACTATTAAAC ACTCTACCCG ACATGTCCAG	360
CACCACTGGT AAGCCTTCTC CAGCCAACAC ACACACACAC ACACNCACAC ACACACATAT	420
CCAGGCACAG GCTACCTCAT CTTCACAAATC ACCCCTTAA TTACCATGCT ATGGTGG	477

## (2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTAAAG AGGGAAGAAC	60
TAACGTATTT TAGAGAGCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAA GGTGGGGCCT	120

GATGATAAAAT AAGAGTCAGC CAGGTAAGTG GGTGGTGTGG TATGGGCACA GTGAAGAAC	180
TTTCAGGCAG AGGAAACAGC AGTAAA	207

## (2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ACCTTGATTT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG	60
CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTTGGG T	111

## (2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 196 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGCGCGGCAG GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTTGATAAC	60
AGCAAGATGG CTTTGAACTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT	120
GGATACCAAC CGGAAAACCC CTATCCCGCA CAGCCCCTG TGTTCCCCAC TGTCTACGAG	180
GTGCATCCGG CTCAGT	196

## (2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 132 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC	60
CTTCCCCCTT TCATCTAGTG GTGGAAACCT GATGCTTTAT GTTGACAGGA ATAGAACCCAG	120
GAGGGAGTTT GT	132

## (2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 285 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ACAAANACCCA NGANAGGCCA CTGGCCGTGG TGTCACTGCC TCCAAACATG AAAGTGTAG	60
CTTCTGCTCT TATGTCCTCA TCTGACAACCT CTTTACCAATT TTTATCCTCG CTCAGCAGGA	120
GCACATCAAT AAAGTCCAAA GTCTTGGACT TGGCCTTGGC TTGGAGGAAG TCATCAACAC	180
CCTGGCTAGT GAGGGTGCAG CGCCGCTCCT GGATGACGGC ATCTGTGAAG TCGTGCACCA	240
GTCTGCAGGC CCTGTGGAAG CGCCGTCCAC ACGGAGTNAG GAATT	285

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ACCACAGTCC TGTGGGCCA GGGCTTCATG ACCCTTTCTG TGAAAAGCCA TATTATCACC	60
ACCCCAAATT TTTCTTAAAT TATCTTTAAC TGAAGGGGTC AGCCTCTTGA CTGCAAAGAC	120
CCTAACGCCGG TTACACAGCT AACTCCCCT GGCCTTGATT TGTGAAATTG CTGCTGCCTG	180
ATTGGCACAG GAGTCGAAGG TGTCAGCTC CCCTCCTCCG TGGAACGAGA CTCTGATTG	240
AGTTTCACAA ATTCTCGGGC CACCTCGTCA TTGCTCCTCT GAAATAAAAT CCGGAGAATG	300
GTCAGGCCTG TCTCATCCAT ATGGATCTTC CGG	333

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAA GATCATCAGG GCATGGATGG	60
GAAAGTGCTT TGGGAACGTG AAAGTGCCTA ACACATGATC GATGATTTT GTTATAATAT	120
TTGAATCACG GTGCATACAA ACTCTCCTGC CTGCTCCTCC TGGGCCAG CCCCAGCCCC	180
ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTGGCT	240

GCTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGT A AGGCATGCTG	300
GCCCTGGT	308

## (2) INFORMATION FOR SEQ ID NO:156:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ACCTTGCTCG GTGCTTGGAA CATATTAGGA ACTCAAATA TGAGATGATA ACAGTGCCTA	60
TTATTGATTA CTGAGAGAAC TGTTAGACAT TTAGTTGAAG ATTTCTACA CAGGAAGTGA	120
GAATAGGAGA TTATGTTGG CCCTCATATT CTCTCCTATC CTCCTTGCT CATTCTATGT	180
CTAATATATT CTCATCAAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT	240
AAAACCAGAT GTCTATCCTT AAGATTTC AATAGAAAAC AAATTAACAG ACTAT	295

## (2) INFORMATION FOR SEQ ID NO:157:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACAAGTTAA ATAGTGCTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTTCT	60
GAAGAGCAAA ACAAAATTCTG TCATGTAATC TCTATCTTGG GTCGTGGGTA TATCTGTCCC	120
CTTAGT	126

## (2) INFORMATION FOR SEQ ID NO:158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ACCCACTGGT CTTGGAAACA CCCATCCTTA ATACGATGAT TTTCTGTCG TGTGAAAATG	60
AANCCAGCAG GCTGCCCTA GTCAGTCCTT CCTTCCAGAG AAAAAGAGAT TTGAGAAAGT	120
GCCTGGGTAA TTCACCATT A TTTCTCTCC CCAAACCTCTC TGAGTCTTCC CTTAATATTT	180

CTGGTGGTTC TGACCAAAGC AGGTCATGGT TTGTTGAGCA TTTGGGATCC CAGTGAAGTA	240
NATGTTGTA GCCTTGCATA CTTAGCCCTT CCCACGCACA AACGGAGTGG CAGAGTGGTG	300
CCAACCCCTGT TTTCCCAGTC CACGTAGACA GATTACAGT GCGGAATTCT GGAAGCTGGA	360
NACAGACGGG CTCTTGCAG AGCCGGGACT CTGAGANGGA CATGAGGGCC TCTGCCTCTG	420
TGTTCATTCT CTGATGTCCT GT	442

## (2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

ACTTCCAGGT AACGTTGTTG TTTCCGTTGA GCCTGAAC TG ATGGGTGACG TTGTAGGTTC	60
TCCAACAAGA ACTGAGGTTG CAGAGCAGGT AGGGAAGAGT GCTGTTCCAG TTGCACCTGG	120
GCTGCTGTGG ACTGTTGTTG ATTCTCTACT ACGGCCAAG GTTGTGGAAC TGGCANAAAG	180
GTGTGTTGTT GGANTTGAGC TCGGGCGGCT GTGGTAGGTT GTGGGCTCTT CAACAGGGC	240
TGCTGTGGTG CGGGGANGTG AANGTGTGTT GTCACTTGAG CTTGGCCAGC TCTGGAAAGT	300
ANTANATTCT TCCTGAAGGC CAGCGCTTGT GGAGCTGGCA NGGGTCANTG TTGTGTGTA	360
CGAACCAAGTG CTGCTGTGGG TGGGTGTANA TCCTCCACAA AGCCTGAAGT TATGGTGT	420
TCAGGTAANA ATGTGGTTTC AGTGTCCCTG GGCNGCTGTG GAAGGTTGTA NATTGTCACC	480
AAGGGAATAA GCTGTGGT	498

## (2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ACCTGCATCC AGCTTCCCTG CCAAACCTCAC AAGGAGACAT CAACCTCTAG ACAGGGAAAC	60
AGCTTCAGGA TACTTCCAGG AGACAGAGCC ACCAGCAGCA AAACAAATAT TCCCATGCCT	120
GGAGCATGGC ATAGAGGAAG CTGANAAATG TGGGGTCTGA GGAAGCCATT TGAGTCTGGC	180
CACTAGACAT CTCATCAGCC ACTTGTGTGA AGAGATGCC CATGACCCCA GATGCCTCTC	240
CCACCCCTAC CTCCATCTCA CACACTTGAG CTTTCCACTC TGTATAATTG TAACATCCTG	300
GAGAAAAATG GCAGTTGAC CGAACCTGTT CACAACGGTA GAGGCTGATT TCTAACGAAA	360
CTTGTAGAAT GAAGCCTGGA	380

## (2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

ACTCCACATC CCCTCTGAGC AGGCGGTTGT CGTTCAAGGT GTATTTGGCC TTGCCTGTCA 60  
CACTGTCCAC TGGCCCCTTA TCCACTTGGT GCTTAATCCC TCGAAAGAGC ATGT 114

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

ACTTTCTGAA TCGAATCAA TGATACTTAG TGTAGTTTA ATATCCTCAT ATATATCAA 60  
GTTTTACTAC TCTGATAATT TTGTAAACCA GGTAACCAGA ACATCCAGTC ATACAGCTT 120  
TGGTGATATA TAACTTGGCA ATAACCCAGT CTGGTGATAC ATAAAACATAC TCACGT 177

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTTATACA GACAGGCGTG AAGACATTCA CGACAAAAAC GCGAAATTCT ATCCCGTGAC 60  
CANAGAAGGC AGCTACGGCT ACTCCTACAT CCTGGCGTGG GTGGCCTTCG CCTGCACCTT 120  
CATCAGCGGC ATGATGT 137

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTTATCACAA TGAATGTTCT CCTGGGCAGC GTTGTGATCT TTGCCACCTT CGTGACTTTA	60
TGCAATGCAT CATGCTATTT CATACTTAAT GAGGGAGTTC CAGGAGATTG AACCAGGAAA	120
TGCATGGATC TCAAAGGAAA CAAACACCCA ATAAACTCGG AGTGGCAGAC TGACAACGT	180
GAGACATGCA CTTGCTACGA AACAGAAATT TCATGTTGCA CCCTTGTTC TACACCTGTG	240
GGTTATGACA AAGACAACTG CCAAAGAACATC TTCAAGAAGG AGGACTGCAA GTATATCGTG	300
GTGGAGAAGA AGGACCCAAA AAAGACCTGT TCTGTCAGTG AATGGATAAT CTAATGTGCT	360
TCTAGTAGGC ACAGGGCTCC CAGGCCAGGC CTCATTCTCC TCTGGCCTCT AATAGTCAAT	420
GATTGTGTAG CCATGCCTAT CAGTAAAAAG ATNTTGAGC AAACACTTT	469

## (2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 195 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

ACAGTTTTT ATANATATCG ACATTGCCGG CACTTGTGTT CAGTTTCATA AAGCTGGTGG	60
ATCCGCTGTC ATCCACTATT CCTTGGCTAG AGTAAAAAATT ATTCTTATAG CCCATGTCCC	120
TGCAGGCCGC CCGCCCGTAG TTCTCGTTCC AGTCGTCTTG GCACACAGGG TGCCAGGACT	180
TCCTCTGAGA TGAGT	195

## (2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 383 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ACATCTTAGT AGTGTGGCAC ATCAGGGGGC CATCAGGGTC ACAGTCACTC ATAGCCTCGC	60
CGAGGTCGGA GTCCACACCA CCGGTGTAAGG TGTGCTCAAT CTTGGGCTTG GCGCCCACCT	120
TTGGAGAAGG GATATGCTGC ACACACATGT CCACAAAGCC TGTGAACCTCG CCAAAGAATT	180
TTTGCAGACC AGCCTGAGCA AGGGGCGGAT GTTCAGCTTC AGCTCCTCCT TCGTCAGGTG	240
GATGCCAACC TCGTCTANGG TCCGTGGGAA GCTGGTGTCC ACNTCACCTA CAACCTGGGC	300
GANGATCTTA TAAAGAGGCT CCNAGATAAA CTCCACGAAA CTTCTCTGGG AGCTGCTAGT	360
NGGGGCCTTT TTGGTGAAC TTC	383

## (2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 247 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT	60
TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC	120
TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGGCAG ANCCAGAGAC	180
TCAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC	240
TGANGTC	247

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

ACTTCTAAGT TTTCTAGAAG TGGAAGGATT GTANTCATCC TGAAAATGGG TTTACTTCAA	60
AATCCCTCAN CCTTGTCTT CACNACTGTC TATACTGANA GTGTCACTGTT TCCACAAAGG	120
GCTGACACCT GAGCCTGNAT TTTCACTCAT CCCTGAGAAG CCCTTTCCAG TAGGGTGGGC	180
AATTCCCAAC TTCCTTGCCA CAAGCTTCCC AGGCTTTCTC CCCTGGAAAA CTCCAGCTTG	240
AGTCCCAGAT ACACCTCATGG GCTGCCCTGG GCA	273

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ACAGCCTTGG CTTCCCCAAA CTCCACAGTC TCAGTGCAGA AAGATCATCT TCCAGCAGTC	60
AGCTCAGACC AGGGTCAAAG GATGTGACAT CAACAGTTTC TGGTTTCAGA ACAGGTTCTA	120
CTACTGTCAA ATGACCCCCC ATACTTCCTC AAAGGCTGTG GTAAGTTTG CACAGGTGAG	180
GGCAGCAGAA AGGGGGTANT TACTGATGGA CACCATCTTC TCTGTATACT CCACACTGAC	240
CTTGGCCATGG GCAAAGGCCCT TACCCACAAA AACAAATAGGA TCACTGCTGG GCACCAGCTC	300
ACGCACATCA CTGACAACCG GGATGGAAAA AGAANTGCCA ACTTTCATAC ATCCAACCTGG	360
AAAGTGATCT GATACTGGAT TCTTAATTAC CTTCAAAAGC TTCTGGGGC CATCAGCTGC	420
TCGAACACTG A	431

(2) INFORMATION FOR SEQ ID NO:170:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ACCTGTGGGC TGGGCTGTTA TGCCTGTGCC GGCTGCTGAA AGGGAGTTCA GAGGTGGAGC	60
TCAAGGAGCT CTGCAGGCAT TTTGCCAANC CTCTCCANAG CANAGGGAGC AACCTACACT	120
CCCCGCTAGA AAGACACCAAG ATTGGAGTCC TGGGAGGGGG AGTTGGGGTG GGCATTTGAT	180
GTATACTTGT CACCTGAATG AANGAGCCAG AGAGGAANGA GACGAANATG ANATTGGCCT	240
TCAAAGCTAG GGGTCTGGCA GGTGGA	266

(2) INFORMATION FOR SEQ ID NO:171:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GGCAGCCAAA TCATAAACGG CGAGGACTGC AGCCCGCACT CGCAGCCCTG GCAGGGGGCA	60
CTGGTCATGG AAAACGAATT GTTCTGCTCG GGCCTCCTGG TGATCCGCA GTGGGTGCTG	120
TCAGCCGCAC ACTGTTCCA GAAAGTGAGTG CAGAGCTCCT ACACCCTCGG GCTGGGCCTG	180
CACAGTCTTG AGGCCGACCA AGAGCCAGGG AGCCAGATGG TGGAGGCCAG CCTCTCCGTA	240
CGGCACCCAG AGTACAACAG ACCCTTGCTC GCTAACGACC TCATGCTCAT CAAGTTGGAC	300
GAATCCGTGT CCGAGTCTGA CACCATCCGG AGCATCAGCA TTGCTTCGCA GTGCCCTACC	360
GCGGGGAACT CTTGCCTCGT TTCTGGCTGG GGTCTGCTGG CGAACGGCAG AATGCCTACC	420
GTGCTGCAGT CGTGAACGT GTCGGTGGTG TCTGAGGAGG TCTGCAGTAA GCTCTATGAC	480
CCGCTGTACC ACCCCAGCAT GTTCTGCGCC GGCAGGGGC AAGACCAGAA GGACTCCTGC	540
AACGGTGAAT CTGGGGGGCC CCTGATCTGC AACGGTACT TGCAAGGCCT TGTGTCTTTC	600
GGAAAAGCCC CGTGTGGCCA AGTTGGCGTG CCAGGTGTCT ACACCAACCT CTGCAAATTC	660
ACTGAGTGGAA TAGAGAAAAC CGTCCAGGCC AGTTAACTCT GGGGACTGGG AACCCATGAA	720
ATTGACCCCC AAATACATCC TGCAGGAAGGA ATTCAAGGAAT ATCTGTTCCC AGCCCCTCCT	780
CCCTCAGGCC CAGGAGTCCA GGCCCCCAGC CCCTCCTCCC TCAAACCAAG GGTACAGATC	840
CCCAGCCCC CCTCCCTCAG ACCCAGGAGT CCAGACCCCC CAGCCCCCTCC TCCCTCAGAC	900
CCAGGAGTCC AGCCCCCTCCT CCCTCAGACC CAGGAGTCCA GACCCCCCAG CCCCTCCTCC	960
CTCAGACCCA GGGGTCCAGG CCCCCAACCC CTCCCTCCCTC AGACTCAGAG GTCCAAGCCC	1020
CCAACCCNTC ATTCCCCAGA CCCAGAGGTC CAGGTCCCAG CCCCTCNTCC CTCAGACCCA	1080
CGGGTCCAAT GCCACCTAGA CTNTCCCTGT ACACAGTGCC CCCTTGTGGC ACGTTGACCC	1140
AACCTTACCA GTTGGTTTT CATTTTNGT CCCTTCCCC TAGATCCAGA AATAAAGTTT	1200
AAGAGAAGNG CAAAAAAAGA AAAAAAAAGA AAAAAAAAGA AAAAAAAAGA	1248

(2) INFORMATION FOR SEQ ID NO:172:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met	Val	Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro
1					5			10					15		
Leu	Leu	Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser
					20			25				30			
Glu	Ser	Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr
				35			40					45			
Ala	Gly	Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Gly
				50			55				60				
Arg	Met	Pro	Thr	Val	Leu	Gln	Cys	Val	Asn	Val	Ser	Val	Val	Ser	Glu
	65				70				75				80		
Glu	Val	Cys	Ser	Lys	Leu	Tyr	Asp	Pro	Leu	Tyr	His	Pro	Ser	Met	Phe
		85				90						95			
Cys	Ala	Gly	Gly	Gly	Gln	Xaa	Gln	Xaa	Asp	Ser	Cys	Asn	Gly	Asp	Ser
		100				105						110			
Gly	Gly	Pro	Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu	Val	Ser	Phe
		115				120						125			
Gly	Lys	Ala	Pro	Cys	Gly	Gln	Val	Gly	Val	Pro	Gly	Val	Tyr	Thr	Asn
		130				135						140			
Leu	Cys	Lys	Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Ala	Ser	
		145				150						155			

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1265 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCAGCCCGC	ACTCGCAGGCC	CTGGCAGGCG	GCACTGGTCA	TGGAAAACGA	ATTGTTCTGC	60
TCGGGCGTCC	TGGTGCATCC	GCAGTGGGTG	CTGTCAGCCG	CACACTGTTT	CCAGAACTCC	120
TACACCATCG	GGCTGGGCCT	GCACAGTCTT	GAGGCCGACC	AAGAGCCAGG	GAGCCAGATG	180
GTGGAGGCCA	GCCTCTCCGT	ACGGCACCCA	GAGTACAACA	GACCCTTGCT	CGCTAACGAC	240

CTCATGCTCA	TCAAGTTGGA	CGAATCCGTG	TCCGAGTCTG	ACACCATCCG	GAGCATCAGC	300
ATTGCTTCGC	AGTGCCTAC	CGCGGGGAAC	TCTTGCCTCG	TTTCTGGCTG	GGGTCTGCTG	360
GCGAACGGTG	AGCTCACGGG	TGTGTGCTG	CCCTCTTCAA	GGAGGTCCTC	TGCCAGTCG	420
CGGGGGCTGA	CCCAGAGCTC	TGCGTCCCAG	GCAGAATGCC	TACCGTGCTG	CAGTGCCTGA	480
ACGTGTCGGT	GGTGTCTGAG	GAGGTCTGCA	GTAAGCTCTA	TGACCCGCTG	TACCAACCCA	540
GCATGTTCTG	CGCCGGCGGA	GGGCAAGACC	AGAAGGACTC	CTGCAACGGT	GACTCTGGGG	600
GGCCCCTGAT	CTGCAACGGG	TACTTGCAGG	GCCTTGTGTC	TTTCGGAAAA	GCCCCGTGTG	660
GCCAAGTTGG	CGTGCCAGGT	GTCTACACCA	ACCTCTGCAA	ATTCACTGAG	TGGATAGAGA	720
AAACCGTCCA	GGCCAGTTAA	CTCTGGGAC	TGGGAACCCA	TGAAATTGAC	CCCCAAATAC	780
ATCCTGCGGA	AGGAATTCAAG	GAATATCTGT	TCCCAGCCCC	TCCTCCCTCA	GGCCCAGGAG	840
TCCAGGGCCC	CAGCCCTCTC	TCCCTCAAAC	CAAGGGTACA	GATCCCCAGC	CCCTCCTCCC	900
TCAGACCCAG	GAGTCCAGAC	CCCCCAGCCC	CTCCTCCCTC	AGACCCAGGA	GTCCAGCCCC	960
TCCTCCNTCA	GACCCAGGAG	TCCAGACCCC	CCAGCCCTC	CTCCCTCAGA	CCCAGGGGTT	1020
GAGGCCCTCA	ACCCCTCTC	CTTCAGAGTC	AGAGGTCAA	GCCCCAACC	CCTCGTTCCC	1080
CAGACCCAGA	GGTNNAAGGT	CCAGCCCTC	TTCCNTCAGA	CCCAGNGTC	CAATGCCACC	1140
TAGATTTC	CTGNACACAG	TGCCCCCTTG	TGGNANGTTG	ACCCAACCTT	ACCAGTTGGT	1200
TTTCATTT	TNGTCCCTT	CCCCTAGATC	CAGAAATAAA	GTTAAGAGA	NGNGCAAAAA	1260
AAAAAA						1265

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GGTCAGCCGC	ACACTGTTTC	CAGAAGTGAG	TGCAGAGCTC	CTACACCATC	GGGCTGGGCC	60
TGCACAGTCT	TGAGGCCGAC	CAAGAGCCAG	GGAGCCAGAT	GGTGGAGGCC	AGCCTCTCCG	120
TACGGCACCC	AGAGTACAAC	AGACCCTTGC	TCGCTAACGA	CCTCATGCTC	ATCAAGTTGG	180
ACGAATCCGT	GTCCGAGTCT	GACACCATCC	GGAGCATCAG	CATTGCTTCG	CAGTGCCCTA	240
CCGCGGGAA	CTCTTGCCTC	GTTTCTGGCT	GGGGTCTGCT	GGCGAACGGT	GAGTCACGG	300
GTGTGTGTCT	GCCCTCTTCA	AGGAGGTCT	CTGCCCAGTC	GCGGGGGCTG	ACCCAGAGCT	360
CTGCGTCCCA	GGCAGAAATGC	CTACCGTGC	GCAGTGCCTG	AACGTGTGG	TGGTGTCTGA	420
NGAGGTCTGC	ANTAAGCTCT	ATGACCCGCT	GTACCACCCC	ANCATGTTCT	GCGCCGGCGG	480
AGGGCAAGAC	CAGAAGGACT	CCTGCAACGT	GAGAGAGGGG	AAAGGGGAGG	GCAGGCGACT	540
CAGGGAAGGG	TGGAGAAGGG	GGAGACAGAG	ACACACAGGG	CCGCATGGCG	AGATGCAGAG	600
ATGGAGAGAC	ACACAGGGAG	ACAGTGACAA	CTAGAGAGAG	AAACTGAGAG	AAACAGAGAA	660
ATAAACACAG	GAATAAAGAG	AAGCAAAGGA	AGAGAGAAAC	AGAAACAGAC	ATGGGGAGGC	720
AGAAACACAC	ACACATAGAA	ATGCAGTTGA	CCTTCCAACA	GCATGGGGCC	TGAGGGCGGT	780
GACCTCCACC	CAATAGAAAA	TCCTCTTATA	ACTTTTGACT	CCCCAAAAAC	CTGACTAGAA	840
ATAGCCTACT	GTTGACGGGG	AGCCTTACCA	ATAACATAAA	TAGTCGATT	ATGCATACGT	900
TTTATGCATT	CATGATATAC	CTTGTGTTGGA	ATTTTTGAT	ATTCTAAGC	TACACAGTTC	960
GTCTGTGAAT	TTTTTAAAT	TGTTGCAACT	CTCCTAAAAT	TTTCTGATG	TGTTTATTGA	1020
AAAAATCCAA	GTATAAGTGG	ACTTGTGCAT	TCAAACCAGG	GTTGTTCAAG	GGTCAACTGT	1080
GTACCCAGAG	GGAAACAGTG	ACACAGATTC	ATAGAGGTGA	AACACGAAGA	GAAACAGGAA	1140
AAATCAAGAC	TCTACAAAGA	GGCTGGGCAG	GGTGGCTCAT	GCCTGTAATC	CCAGCACTTT	1200
GGGAGGCGAG	GCAGGGCAGAT	CACTTGAGGT	AAGGAGTTCA	AGACCAGCCT	GGCCAAAATG	1260
GTGAAATCCT	GTCTGTACTA	AAAATACAAA	AGTTAGCTGG	ATATGGTGGC	AGGCGCCTGT	1320
AATCCCAGCT	ACTTGGGAGG	CTGAGGCAGG	AGAATTGCTT	GAATATGGGA	GGCAGAGGTT	1380
GAAGTGAGTT	GAGATCACAC	CACTATACTC	CAGCTGGGGC	AACAGAGTAA	GACTCTGTCT	1440
AAAAAAAAAA	AAAAAAAAAA					1459

(2) INFORMATION FOR SEQ ID NO:175:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GCGCAGCCCT	GGCAGGCGGC	ACTGGTCATG	GAAAACGAAT	TGTTCTGCTC	GGGCGTCCTG	60
GTGCATCCGC	AGTGGGTGCT	GTCAGCCGCA	CACTGTTCC	AGAACTCCTA	CACCATCGGG	120
CTGGGCCTGC	ACAGTCTTGA	GGCCGACCAA	GAGCCAGGGA	GCCAGATGGT	GGAGGCCAGC	180
CTCTCCGTAC	GGCACCCAGA	GTACAACAGA	CTCTTGCTCG	CTAACGACCT	CATGCTCATC	240
AAGTTGGACG	AATCCGTGTC	CGAGTCTGAC	ACCATCCGGA	GCATCAGCAT	TGCTTCGAG	300
TGCCCTACCG	CGGGGAACTC	TTGCCTCGTN	TCTGGCTGGG	GTCTGCTGGC	GAACGGCAGA	360
ATGCCTACCG	TGCTGCACTG	CGTGAACGTG	TCGGTGGTGT	CTGAGGAGNT	CTGCAGTAAG	420
CTCTATGACC	CGCTGTACCA	CCCCAGCATG	TTCTGCGCCG	GCGGAGGGCA	AGACCCAGAAG	480
GACTCCTGCA	ACGGTGACTC	TGGGGGGCCC	CTGATCTGCA	ACGGGTACTT	GCAGGGCCTT	540
GTGTCTTCG	GAAAAGCCCC	GTGTGCCAA	CTTGGCGTGC	CAGGTGTCTA	CACCAACCTC	600
TGCAAATTCA	CTGAGTGGAT	AGAGAAAACC	GTCCAGNCCA	GTAACTCTG	GGGACTGGGA	660
ACCCATGAAA	TTGACCCCCA	AATACATCCT	GCGGAANGAA	TTCAGGAATA	TCTGTTCCCA	720
GCCCCCTCCTC	CCTCAGGCC	AGGAGTCCAG	GCCCCCAGCC	CCTCCTCCCT	CAAACCAAGG	780
GTACAGATCC	CCAGCCCCTC	CTCCCTCAGA	CCCAGGAGTC	CAGACCCCCC	AGCCCCCTCNT	840
CCNTCAGACC	CAGGAGTCCA	GCCCCCTCCTC	CNTCAGACGC	AGGAGTCCAG	ACCCCCCAGC	900
CCNTCNTCCG	TCAGACCCAG	GGGTGCAGGC	CCCCAACCCC	TCNTCCNTCA	GAGTCAGAGG	960
TCCAAGCCCC	CAACCCCTCG	TTCCCCAGAC	CCAGAGGTNC	AGGTCCCAGC	CCCTCCTCCC	1020
TCAGACCCAG	CGGTCCAATG	CCACCTAGAN	TNTCCCTGTA	CACAGTGCC	CCTTGTGGCA	1080
NGTTGACCCA	ACCTTACCAAG	TTGGTTTTTC	ATTTTTGTC	CCTTCCCCCT	AGATCCAGAA	1140
ATAAAAGNTA	AGAGAAGCGC	AAAAAAA				1167

## (2) INFORMATION FOR SEQ ID NO:176:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp
1				5					10				15		

Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu
				20					25				30		

Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
				35				40				45			

Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Leu	Leu	
				50				55			60				

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser  
 65 70 75 80  
 Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly  
 85 90 95  
 Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met  
 100 105 110  
 Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val  
 115 120 125  
 Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala  
 130 135 140  
 Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly  
 145 150 155 160  
 Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys  
 165 170 175  
 Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys  
 180 185 190  
 Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser  
 195 200 205

## (2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1119 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GC	GC	ACT	TC	GC	AG	CC	CT	GG	CA	GG	CC	AA	CT	AT	GG	AA	AC	GA	AT	TT	GT	TT	CT	GC	GG	GC	60
G	T	C	C	T	G	C	A	T	G	G	C	A	C	T	G	C	A	G	T	T	G	T	C	T	C	G	120
A	T	C	C	G	C	T	G	A	C	C	G	A	G	A	C	T	C	A	G	A	G	T	T	G	T	G	180
T	C	G	G	C	T	C	A	T	G	A	G	G	A	G	C	T	G	C	T	A	G	T	C	T	C	T	240
C	T	A	A	G	T	C	G	T	C	G	A	C	T	A	C	T	G	C	T	A	G	T	T	G	T	G	300
G	A	A	T	T	C	T	G	C	T	T	T	C	T	T	T	G	G	G	G	T	T	T	G	G	G	A	360
C	A	A	C	C	T	C	G	G	G	G	A	G	A	G	C	T	G	A	G	T	T	T	T	T	T	T	420
A	A	C	C	T	C	G	G	G	G	G	A	G	A	G	C	T	G	A	G	T	T	T	T	T	T	T	480
T	G	A	A	T	C	T	G	C	T	T	T	C	T	A	C	T	G	A	G	T	T	T	T	T	T	T	540
G	T	C	C	A	T	G	C	T	C	T	G	A	G	T	G	A	T	C	A	T	G	T	T	T	T	T	600
C	A	A	C	C	T	C	G	G	G	G	A	G	A	G	C	T	G	A	G	T	T	T	T	T	T	T	660
A	G	T	T	T	C	T	G	C	T	T	T	C	T	T	T	G	G	G	G	T	T	T	T	T	T	T	720
T	G	A	A	T	C	T	G	C	T	T	T	C	T	T	T	G	G	G	G	T	T	T	T	T	T	T	780
G	G	T	T	T	C	T	G	C	T	T	T	C	T	T	T	G	G	G	G	T	T	T	T	T	T	T	840
G	G	T	T	T	C	T	G	C	T	T	T	C	T	T	T	G	G	G	G	T	T	T	T	T	T	T	900
A	C	A	C	T	C	T	G	C	T	T	T	C	T	T	T	G	G	G	G	T	T	T	T	T	T	T	960
A	C	A	C	T	C	T	G	C	T	T	T	C	T	T	T	G	G	G	G	T	T	T	T	T	T	T	1020
G	A	G	G	T	A	T	G	C	T	T	T	C	T	T	T	G	G	G	G	T	T	T	T	T	T	T	1080

TTAATAAACAA GAAGCTGTGA TGTTAAAAAA AAAAAAAA

1119

## (2) INFORMATION FOR SEQ ID NO:178:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp
1				5					10			15			

Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu
					20			25				30			

Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
				35			40			45					

Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro	Leu	Leu
				50			55			60					

Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu	Ser
	65				70			75			80				

Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala	Gly
	85				90					95					

Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Asp	Ala	Val
				100				105			110				

Ile	Ala	Ile	Gln	Ser	Xaa	Thr	Val	Gly	Gly	Trp	Glu	Cys	Glu	Lys	Leu
			115				120			125					

Ser	Gln	Pro	Trp	Gln	Gly	Cys	Thr	Ile	Ser	Ala	Thr	Ser	Ser	Ala	Arg
	130				135					140					

Thr	Ser	Cys	Cys	Ile	Leu	Thr	Gly	Cys	Ser	Leu	Leu	Leu	Thr	Ala	Ser
145				150					155			160			

Pro	Gly	Thr	Leu												
-----	-----	-----	-----	--	--	--	--	--	--	--	--	--	--	--	--

## (2) INFORMATION FOR SEQ ID NO:179:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGCC TTGGTGTTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT

60

CCAGCTGCC	CCGGCCGGGG	GATGCGAGGC	TCGGAGCACC	CTTGCCTGGC	TGTGATTGCT	120
GCCAGGCACT	GTCATCTCA	GCTTTCTGT	CCCTTGCTC	CCGGCAAGCG	CTTCTGCTGA	180
AAGTCATAT	CTGGAGCCTG	ATGTCTAAC	GAATAAAGGT	CCCATGCTCC	ACCCGAAAAA	240
AAAAAAAAAA						250

## (2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGCCAA	CACAATGGCT	ACCTTTAACAA	60
TCACCCAGAC	CCCGCCCCCTG	CCCGTCCCCC	ACGCTGCTGC	TAACGACAGT	ATGATGCTTA	120
CTCTGCTACT	CGGAAACTAT	TTTATGTAA	TTAATGTATG	CTTCTTGTT	TATAAATGCC	180
TGATTTAAAA AAAAAAAAAA AA						202

## (2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCYTTGKT	NAGGTTTKKG	AGACAMCCCK	AGACCTWAAN	CTGTGTCACA	GACTTCYNGG	60
AATGTTTAGG	CAGTGCTAGT	AATTCYTCG	TAATGATTCT	GTTATTACTT	TCCTNATTCT	120
TTATTCTCT	TTCTTCTGAA	GATTAATGAA	GTTGAAAATT	GAGGTGGATA	AATACAAAAA	180
GGTAGTGTGA	TAGTATAAGT	ATCTAAGTGC	AGATGAAAGT	GTGTTATATA	TATCCATTCA	240
AAATTATGCA	AGTTAGTAAT	TACTCAGGGT	TAACTAAATT	ACTTTAATAT	GCTGTTGAAC	300
CTACTCTGTT	CCTTGGCTAG	AAAAAATTAT	AAACAGGACT	TTGTTAGTT	GGGAAGCCAA	360
ATTGATAATA	TTCTATGTT	AAAAAGTTGG	GCTATACATA	AATTATTAAG	AAATATGGAW	420
TTTTTATTCCC	AGGAATATGG	KGTTCATTT	ATGAATATTA	CSCRGGATAG	AWGTWTGAGT	480
AAAAYCAGTT TTGGTWAATA YGTWAATATG TCMTAAATAA ACAAKGCTTT GACTTATTTC						540
CAAAAAAAAAA AAAAAAAAAA						558

## (2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ACAGGGWTTK	GRGGATGCTA	AGSCCCRG	RWTYGT	TCCAACCCTG	GCTTWTTTTC	60
AGAGGGAAA	ATGGGGCCTA	GAAGTTACAG	MSCATYTAGY	TGGTGC	GMTG GCACCCCTGG	120
CSTCACACAG	ASTCCCGAGT	AGCTGGACT	ACAGGCACAC	AGTC	ACTGAA GCAGGCCCTG	180
TTWGCAATT	ACGTTGCCAC	CTCCA	AACTTCTTC	ATATGTGATG	TCCTTAGTCA	240
CTAAGGTTAA	ACTTTCCCAC	CCAGAAAAGG	CAACTTAGAT	AAAATCTTAG	AGTACTTTCA	300
TACTMTTCTA	AGTCCTCTTC	CAGCCTCACT	KKGAGTC	CTM CYTGGGGTT	GATAGGAANT	360
NTCTCTTGGC	TTTCTCAATA	AARTCTCTAT	YCATCTCATG	TTTAATTG	GG TACGCATARA	420

AWTGSTGARA AAATTAAAAT GTTCTGGTTY MACTTTAAAAA ARAAAAAAAA AAAAAAAA

479

(2) INFORMATION FOR SEQ ID NO:183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

AGGCAGGGAGC	AGAAGCTAAA	GCCAAAGCCC	AAGAAGAGTG	GCAGTGCCAG	CACTGGTGCC	60
AGTACCAAGTA	CCAATAACAG	TGCCAGTGCC	AGTGCCAGCA	CCAGTGGTGG	CTTCAGTGCT	120
GGTGCCAGCC	TGACCGCCAC	TCTCACATT	GGGCTCTTCG	CTGGCCTTGG	TGGAGCTGGT	180
GCCAGCACCA	GTGGCAGCTC	TGGTGCCTGT	GGTTTCTCCT	ACAAGTGAGA	TTTTAGATAT	240
TGTTAACCTT	GCCAGTCTTT	CTCTTCAAGC	CAGGGTGCAT	CCTCAGAAAC	CTACTCAACA	300
CAGCACTCTA	GGCAGCCACT	ATCAATCAAT	TGAAGTTGAC	ACTCTGCATT	ARATCTATT	360
GCCATTCAA	AAAAAAA	AAAAA				384

(2) INFORMATION FOR SEQ ID NO:184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCGAATTGG	GACCGCTGGC	TTATAAGCGA	TCATGTYNT	CCRGATKAC	CTCAACGAGC	60
AGGGAGATCG	AGTCTATACG	CTGAAGAAAT	TTGACCCGAT	GGGACAACAG	ACCTGCTCAG	120
CCCATCCTGC	TCGGTTCTCC	CCAGATGACA	AATACTCTSG	ACACCGAATC	ACCATCAAGA	180
AACGCTTCAA	GGTGCTCATG	ACCCAGCAAC	CGCGCCCTGT	CCTCTGAGGG	TCCCTTAAAC	240
TGATGTCTTT	TCTGCCACCT	GTTACCCCTC	GGAGACTCCG	TAACCAAAC	CTTCGGACTG	300
TGAGCCCTGA	TGCCTTTTG	CCAGCCATAC	TCTTTGGCAT	CCAGTCTCTC	GTGGCGATTG	360
ATTATGCTTG	TGTGAGGCCAA	TCATGGTGGC	ATCACCCATA	AAGGAAACAC	ATTTGACTTT	420
TTTTTCTCAT	ATTTTAAATT	ACTACMAGAW	TATTWMAGAW	WAAATGAWTT	GAAAAACTST	480
TAAAAAAA	AAAAA					496

(2) INFORMATION FOR SEQ ID NO:185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GCTGGTAGCC	TATGGCGKGG	CCCACGGAGG	GGCTCCTGAG	GCCACGGRAC	AGTGACTTCC	60
CAAGTATCYT	GCGCGCGTC	TTCTACCGTC	CCTACCTGCA	GATCTTCGGG	CAGATTCCCC	120
AGGAGGACAT	GGACGTGGCC	CTCATGGAGC	ACAGCAACTG	YTCGTGGAG	CCCGGCTTCT	180
GGGCACACCC	TCCTGGGGCC	CAGGCGGGCA	CCTGCGTCTC	CCAGTATGCC	AACTGGCTGG	240
TGGTGTGCT	CCTCGTCATC	TTCTGCTCG	TGGCCAACAT	CCTGCTGGTC	AACTTGCTCA	300
TTGCCATGTT	CAGTTACACA	TTCGGCAAAG	TACAGGGCAA	CAGCGATCTC	TACTGGGAAG	360
GCGCAGCGTT	ACCGCCTCAT	CCGG				384

## (2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAGTTAGCTC	CTCCACAAACC	TTGATGAGGT	CGTCTGCAGT	GGCCTCTCGC	TTCATACCGC	60
TNCCATCGTC	ATACTGTAGG	TTTGCCACCA	CYTCCTGGCA	TCTTGGGGCG	GCNTAATATT	120
CCAGGAAACT	CTCAATCAAG	TCACCGTCGA	TGAAACCTGT	GGGCTGGTTC	TGTCTCCGC	180
TCGGTGTGAA	AGGATCTCCC	AGAAGGAGTG	CTCGATCTTC	CCCACACTTT	TGATGACTTT	240
ATTGAGTCGA	TTCTGCATGT	CCAGCAGGAG	GTTGTACCAAG	CTCTCTGACA	GTGAGGTCAC	300
CAGCCCTATC	ATGCCGTTGA	MCGTGCCGAA	GARCACCGAG	CCTTGTGTGG	GGGKKGAAAGT	360
CTCACCCAGA	TTCTGCATTA	CCAGAGAGCC	GTGGCAAAAG	ACATTGACAA	ACTCGCCCAG	420
GTGGAAAAAG	AMCAMCTCCT	GGARGTGCTN	GCCGCTCCTC	GTCMGTGGT	GGCAGCGCTW	480
TCCTTTGAC	ACACAAACAA	GTTAAAGGCA	TTTCAGCCC	CCAGAAANTT	GTCATCATCC	540
AACATNTCGC	ACAGCACTNA	TCCAGTTGGG	ATTAAAT			577

## (2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

AACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGATN	TTGTCTGSTG	AGAATYCATW	60
ACTKGAAAAA	GMAACATTAA	AGCCTGGACA	CTGGTATTAA	AATTACAAT	ATGCAACACT	120
TTAAACAGTG	TGTCAATCTG	CTCCCYYNAC	TTTGTCACTCA	CCAGTCTGGG	AAKAAGGGTA	180
TGCCCTATTC	ACACCTGTTA	AAAGGGCGCT	AAGCATTTTT	GATTCAACAT	CTTTTTTTT	240
GACACAAGTC	CGAAAAAAAGC	AAAAGTAAAC	AGTTATYAAT	TTGTTAGCCA	ATTCACTTTC	300
TTCATGGGAC	AGAGCCATYT	GATTTAAAAA	GCAAATTGCA	TAATATTGAG	CTTYGGGAGC	360
TGATATTGTA	GCGGAAGAGT	AGCCTTCTA	CTTCACCAGA	CACAACTCCC	TTTCATATTG	420
GGATGTTNAC	NAAAGTWATG	TCTCTWACAG	ATGGGATGCT	TTTGTGGCAA	TTCTGTTCTG	480
AGGATCTCCC	AGTTTATTAA	CCACTTGCAC	AAGAAGGCGT	TTTCTTCCTC	AGGC	534

## (2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

AGAAACCACT	ATCTCTNAAA	ACAACCTCTC	ATACCTTGTG	GACCTAATTT	TGTGTGCGTG	60
TGTGTGTGCG	CGCATATTAT	ATAGACAGGC	ACATCTTTT	TACTTTGTA	AAAGCTTATG	120
CCTCTTTGGT	ATCTATATCT	GTGAAAGTTT	TAATGATCTG	CCATAATGTC	TTGGGGACCT	180
TTGTCTTCTG	TGTAAATGGT	ACTAGAGAAA	ACACCTATNT	TATGAGTCAA	TCTAGTTNGT	240
TTTATTCGAC	ATGAAGGAAA	TTTCCAGATN	ACAACACTNA	CAAACCTCTCC	CTKGACKARG	300
GGGGACAAAG	AAAAGCAAAA	CTGAMCATAA	RAAACAAATWA	CCTGGTGAGA	ARTTGCATAA	360
ACAGAAATWR	GGTAGTATAT	TGAARNACAG	CATCATTAAA	RMGTTWTKTT	WTCTCCCTT	420

GCAAAAAACA	TGTACNGACT	TCCC GTTGAG	TAATGCCAAG	TTGTTTTTT	TATNATAAAA	480
CTTGCCTTC	ATTACATGTT	TNAAAGTGGT	GTGGTGGGCC	AAAATATTGA	AATGATGGAA	540
CTGACTGATA	AAGCTGTACA	AATAAGCAGT	GTGCCTAACCA	AGCAACACAG	TAATGTTGAC	600
ATGCTTAATT	CACAAATGCT	AATTCATTA	TAAATGTTG	CTAAAATACA	CTTGAACTA	660
TTTTCTGTN	TTCCCAGAGC	TGAGATNTA	GATTTATGT	AGTATNAAGT	GAAAAANTAC	720
GAAAATAATA	ACATTGAAGA	AAAANANAAA	AAANAAAAAA	A		761

## (2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TTTTTTTTTT	TTTGCCGATN	CTACTATTTT	ATTGCAGGAN	GTGGGGGTGT	ATGCACCGCA	60
CACCGGGGCT	ATNAGAAGCA	AGAAGGAAGG	AGGGAGGGCA	CAGCCCCTTG	CTGAGCAACA	120
AAGCCGCCTG	CTGCCTTCTC	TGTCTGTCTC	CTGGTGCAGG	CACATGGGA	GACCTTCCCC	180
AAGGCAGGGG	CCACCAGTCC	AGGGGTGGGA	ATACAGGGGG	TGGGANGTGT	GCATAAGAAG	240
TGATAGGCAC	AGGCCACCCG	GTACAGACCC	CTCGGCTCCT	GACAGGTNGA	TTTCGACCAAG	300
GTCATTGTGC	CCTGCCAGG	CACAGCGTAN	ATCTGGAAAA	GACAGAATGC	TTTCCTTTTC	360
AAATTTGGCT	NGTCATNGAA	NGGGCANTTT	TCCAANTNG	GCTNGGTCTT	GGTACNCTTG	420
GTTCGGCCCA	GCTCCNCGTC	CAAAAANTAT	TCACCCNNCT	CCNAATTGCT	TGCNGGNCCC	480
CC						482

## (2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TTTTTTTTTT	TTTTAAAACA	GTTTTTCACA	ACAAAATTAA	TTAGAAGAAT	AGTGGTTTG	60
AAAACCTCTCG	CATCCAGTGA	GAAC TACCAT	ACACCACATT	ACAGCTNGGA	ATGTNCTCCA	120
AATGTCTGGT	CAAATGATAC	AATGGAACCA	TTCAATCTTA	CACATGCACG	AAAGAACAAAG	180
CGCTTTGAC	ATACAATGCA	CAAAAAAAA	AGGGGGGGGG	GACCACATGG	ATTAAAATTT	240
TAAGTACTCA	TCACATACAT	TAAGACACAG	TTCTAGTCCA	GTCNAAAATC	AGAACTGCNT	300
TGAAAAATT	CATGTATGCA	ATCCAACCAA	AGAACTTNAT	TGGTGATCAT	GANTNCTCTA	360
CTACATCNAC	CTTGATCATT	GCCAGGAACN	AAAAGTTNAA	ANCACNCNGT	ACAAAAANAA	420
TCTGTAATTN	ANTTCAACCT	CCGTACNGAA	AAATNTTNNT	TATACACTCC	C	471

## (2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAGGGATTGA	AGGTCTGTT	TASTGTCGGM	CTGTTCAGCC	ACCAACTCTA	ACAAGTTGCT	60
GTCTTCCACT	CACTGTCTGT	AAGCTTTTA	ACCCAGACWG	TATCTTCATA	AATAGAACAA	120

ATTCTTCACC AGTCACATCT TCTAGGACCT TTTGGATT AGTTAGTATA AGCTCTCCA	180
CTTCCTTGT TAAGACTTCA TCTGGTAAAG TCTTAAGTT TGTAGAAAGG AATTYAATTG	240
CTCGTTCTCT AACAAATGTCC TCTCCTGAA GTATTGGCT GAACAACCCA CCTAAAGTCC	300
CTTGTGCAT CCATTTAAA TATACTTAAT AGGGCATTGK TNCACTAGGT TAAATTCTGC	360
AAGAGTCATC TGTCTGCAAA AGTTGCGTTA GTATATCTGC CA	402

## (2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGCTCGGAT CCAATAATCT TTGCTTGAGG GCAGCACACA TATNCAGTGC CATGGNAACT	60
GGTCTACCCC ACATGGGAGC AGCATGCCGT AGNTATATAA GGTCAATTCCC TGAGTCAGAC	120
ATGCYTYTTT GAYTACCGTG TGCCAAGTGC TGGTGATTCT YAACACACYT CCATCCCGYT	180
CTTTGTGGA AAAACTGGCA CTTKCTGGA ACTAGCARGA CATCACTTAC AAATTACCCC	240
ACGAGACACT TGAAAGGTGT AACAAAGCGA YTCTTGCATT GCTTTTGTC CCTCCGGCAC	300
CAGTTGTCAA TACTAACCCG CTGGTTGCC TCCATCACAT TTGTGATCTG TAGCTCTGGA	360
TACATCTCCT GACAGTACTG AAGAACTTCT TCTTTGTTT CAAAAGCARC TCTTGGTGCC	420
TGTTGGATCA GGTTCCCATT TCCCAGTCYG AATGTTCACA TGGCATATTT WACTTCCCAC	480
AAAACATTGC GATTGAGGC TCAGCAACAG CAAATCCTGT TCCGGCATTG GCTGCAAGAG	540
CCTCGATGTA GCCGGCCAGC GCCAAGGCAG GCGCCGTGAG CCCAACCAAGC AGCAGAAGCA	600
G	601

## (2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATACAGCCCA NATCCCACCA CGAAGATGCG CTTGTTGACT GAGAACCTGA TGCAGTCAGT	60
GGTCCCGCTG TAGCCCCAGC GACTCTCCAC CTGCTGGAAG CGGTTGATGC TGCACTCYTT	120
CCCAACGCAG GCAGMAGCGG GSCTGGTCAA TGAACCTCCAY TCGTGGCTTG GGGTKGACGG	180
TKAAGTGCAG GAAGAGGCTG ACCACCTCGC GGTCCACCAAG GATGCCCGAC TGTGCGGGAC	240
CTGCAGCGAA ACTCCTCGAT GGTCAATGAGC GGGAAAGCGAA TGAGGCCAG GGCCTTGCCC	300
AGAACCTTCC GCCTGTTCTC TGGCGTCACC TGCAGCTGCT GCGCTGACA CTCGGCCTCG	360
GACCAGCGGA CAAACGGCRT TGAACAGCCG CACCTCACGG ATGCCAGTG TGTGCGCTC	420
CAGGAMMGSC ACCAGCGTGT CCAGGTCAAT GTCGGTGAAG CCCTCCGCGG GTRATGGCGT	480
CTGCAGTGTT TTTGTCGATG TTCTCCAGGC ACAGGCTGGC CAGCTGCGGT TCATCGAAGA	540
GTCGCGCCTG CGTGAGCAGC ATGAAGGCAGT TGTCGGCTCG CAGTTCTTCT TCAGGAACTC	600
CACGCAAT	608

## (2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAACGGCTGG	ACCTTGCCTC	GCATTGTGCT	TGCTGGCAGG	GAATACCTTG	GCAAGCAGYT	60
CCAGTCGAG	CAGCCCCAGA	CCGCTGCCGC	CCGAAGCTAA	GCCTGCCTCT	GGCCTTCCCC	120
TCCGCCTCAA	TGCAGAACCA	GTAGTGGGAG	CACTGTGTTT	AGAGTTAAGA	GTGAACACTG	180
TTTGATTTA	CTTGGGAATT	TCCTCTGTTA	TATAGCTTTT	CCCAATGCTA	ATTTCACAAAC	240
AACAACAACA	AAATAACATG	TTTGCCTGTT	AAGTTGTATA	AAAGTAGGTG	ATTCTGTATT	300
TAAAGAAAAT	ATTACTGTTA	CATATACTGC	TTGCAATTTC	TGTATTTATT	GKTNCTSTGG	360
AAATAAATAT	AGTTATTAAA	GGTTGTCANT	CC			392

## (2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCSTTKGAGG	GGTKAGGKYC	CAGTTYCCGA	GTGGAAGAAA	CAGGCCAGGA	GAAGTGCCTG	60
CCGAGCTGAG	GCAGATGTT	CCACAGTGAC	CCCCAGAGCC	STGGGSTATA	GTYTCTGACC	120
CCTCNCAAGG	AAAGACCACS	TTCTGGGAC	ATGGGCTGGA	GGGCAGGACC	TAGAGGCACC	180
AAGGGAAGGC	CCCATTCCGG	GGSTGTTCCC	CGAGGAGGAA	GGGAAGGGGC	TCTGTGTGCC	240
CCCCASGAGG	AAGAGGCCCT	GAGTCCTGGG	ATCAGACACC	CCTTCACGTG	TATCCCCACA	300
CAAATGCAAG	CTCACCAAGG	TCCCCTCTCA	GTCCCCTTCC	STACACCCTG	AMCGGCCACT	360
GSCSCACACC	CACCCAGAGC	ACGCCACCCG	CCATGGGAR	TGTGCTCAAG	GARTCGCNGG	420
GCARCGTGG	CATCTNGTCC	CAGAAGGGGG	CAGAATCTCC	AATAGANGGA	CTGARCMSTT	480
GCTNANAAAA	AAAAANAAAA	AA				502

## (2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGTTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACCATT	TTGTCTGCTC	60
CCTCTGGAAG	CCTTGCAG	AGCGGACTTT	GTAATTGTTG	GAGAATAACT	GCTGAATTT	120
WAGCTGTTK	GAGTTGATTS	GCACCACTGC	ACCCACAACT	TCAATATGAA	AACYAWTTGA	180
ACTWATTTAT	TATCTGTGA	AAAGTATAAC	AATGAAAATT	TTGTTCATAC	TGTATTKATC	240
AAAGTATGATG	AAAAGCAAWA	GATATATATT	CTTTTATTAT	GTTAAATTAT	GATTGCCATT	300
ATTAATCGGC	AAAATGTGGA	GTGTATGTT	TTTCACAGT	AATATATGCC	TTTTGTAAC	360
TCACCTGGTT	ATTTATTGT	AAATGARTTA	CAAAATTCTT	AATTTAAGAR	AATGGTATGT	420
WATATTTATT	TCATTAATT	CTTCCCTKGT	TTACGTWAAT	TTGAAAAGA	WTGCATGATT	480
TCTTGACAGA	AATCGATCTT	GATGCTGTGG	AAGTAGTTG	ACCCACATCC	CTATGAGTT	540
TTCTTAAAGAT	GTATAAAGGT	TGTAGCCAT	CNAACTTCAA	AGAAAAAAAT	GACCACATAC	600
TTTGCATCA	GGCTGAAATG	TGGCATGCTN	TTCTAATTCC	AACTTTATAA	ACTAGCAAAN	660
	AAGTG					665

## (2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTTTNTTTTT	TTTTTTTG	AGGAAGGATT	CCATTTATTG	TGGATGCATT	TTCACAATAT	60
ATGTTTATTG	GAGCGATCCA	TTATCAGTGA	AAAGTATCAA	GTGTTATAA	NATTTTAGG	120
AAGGCAGATT	CACAGAACAT	GCTNGTCNGC	TTGCAGTTT	ACCTCGTANA	GATNACAGAG	180
AATTATAGTC	NAACCAGTAA	ACNAGGAATT	TACTTTCAA	AAGATTAAT	CCAAACTGAA	240
CAAATTCTA	CCCTGAAACT	TACTCCATCC	AAATATTGGA	ATAANAGTCA	GCAGTGATAC	300
ATTCTCTTCT	GAACTTAGA	TTTCTAGAA	AAATATGTAA	TAGTGATCAG	GAAGAGCTCT	360
TGTTCAAAAG	TACAACNAAG	CAATGTTCCC	TTACCATAGG	CCTTAATTCA	AACTTTGATC	420
CATTCACTC	CCATCACGGG	AGTCAATGCT	ACCTGGGACA	CTTGTATTT	GTTCATNCTG	480
ANCNTGGCTT	AA					492

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTTNTTTG	ATTCANTCT	GTANNAANTA	TTTCATTAT	GTTTATTANA	AAAATATNAA	60
TGTNTCCACN	ACAAATCATN	TTACNTNAGT	AAGAGGCCAN	CTACATTGTA	CAACATACAC	120
TGAGTATATT	TTGAAAAGGA	CAAGTTAAA	GTANACNCAT	ATTGCCGANC	ATANCACATT	180
TATACATGGC	TTGATTGATA	TTTAGCACAG	CANAAACTGA	GTGAGTTACC	AGAAANAAAT	240
NATATATGTC	AATCNGATTT	AAGATACAAA	ACAGATCCTA	TGGTACATAN	CATCNTGTAG	300
GAGTTGTGGC	TTTATGTTA	CTGAAAGTCA	ATGCAGTTCC	TGTACAAAGA	GATGCCGTA	360
AGCATTCTAG	TACCTCTACT	CCATGGTTAA	GAATCGTACA	CTTATGTTA	CATATGTNCA	420
GGGTAAGAAT	TGTGTTAAGT	NAANTTATGG	AGAGGTCCAN	GAGAAAAATT	TGATNCAA	478

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

AGTGACTTGT	CCTCCAACAA	AACCCCTTGA	TCAAGTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTCC	TGTCATCTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGGCA	120
TCAACTCCAG	CTGGATTATT	TTGGAGCCTG	CAAATCTATT	CCTACTTGTA	CGGACTTTGA	180
AGTGATTCA	TTTCCTCTAC	GGATGAGAGA	CTGGCTCAAG	AATATCCTCA	TGCAGCTTTA	240
TGAAGCCNAC	TCTGAACACG	CTGGTTATCT	NAGATGAGAA	NCAGAGAAAT	AAAGTCNAGA	300
AAATTACCT	GGANGAAAAG	AGGCTTNGG	CTGGGGACCA	TCCCATTGAA	CCTTCTCTTA	360
ANGGACTTTA	AGAANAAAAT	ACCACATGTN	TGTNGTATCC	TGGTGCCNGG	CCGTTTANTG	420
AACNTNGACN	NCACCCTNT	GGAATANANT	CTTGACNGCN	TCCTGAACCT	GCTCCTCTGC	480
GA						482

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CGGCCGCAAG	TGCAACTCCA	GCTGGGGCCG	TGCGGACGAA	GATTCTGCCA	GCAGTTGGTC	60
CGACTGCGAC	GACGGCGCG	GCGACAGTCG	CAGGTGCAGC	GCAGGGCGCCT	GGGGTCTTGC	120
AAGGCTGAGC	TGACGCCGCA	GAGGTCGTGT	CACGTCCCAC	GACCTTGACG	CCGTCGGGGA	180
CAGCCGGAAC	AGAGCCCGGT	GAANGCGGG	GGCCTCGGGG	AGCCCCTCGG	GAAGGGCGGC	240
CCGAGAGATA	CGCAGGTGCA	GGTGGCCGCC				270

## (2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TTTTTTTTTT	TTTTGGAATC	TACTGCGAGC	ACAGCAGGTC	AGCAACAAGT	TTATTTGCA	60
GCTAGCAAGG	TAACAGGGTA	GGGCATGGTT	ACATGTTCA	GTCAACTTCC	TTTGTCTGG	120
TTGATTGGTT	TGTCTTATG	GGGGCGGGGT	GGGGTAGGGG	AAANCGAAGC	ANAANTAAACA	180
TGGAGTGGGT	GCACCCCTCCC	TGTAGAACCT	GGTTACNAAA	GCTTGGGGCA	GTTCACCTGG	240
TCTGTGACCG	TCATTTCTT	GACATCAATG	TTATTAGAAG	TCAGGATATC	TTTTAGAGAG	300
TCCACTGTNT	CTGGAGGGAG	ATTAGGGTTT	CTTGCANA	TCCAANCAAA	ATCCACNTGA	360
AAAAGTTGGA	TGATNCANGT	ACNGAATACC	GANGGCATAN	TTCTCATANT	CGGTGGCCA	419

## (2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TTTNTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TGGCACTTAA	TCCATTTTA	TTTCAAATG	TCTACAAANT	TTNAATNCNC	CATTATACNG	120
GTNATTTCNC	AAAATCTAAA	NNTTATTCAA	ATNTNAGCCA	AANTCCTTAC	NCAAATNNAA	180
TACNCNAAA	AATCAAAAT	ATACNTNTCT	TTCAGCAAAC	TTNGTTACAT	AAATTAAAAAA	240
AATATATACG	GCTGGTGT	TCAAAGTACA	ATTATCTTAA	CACTGCAAAC	ATNTTNNA	300
GGAACAAAAA	TAAAAAA	CACTNCCGCA	AAGGTTAAAG	GGAACAAACAA	ATTCTTTA	360
CAACANCNC	NATTATAAAA	ATCATATCTC	AAATCTTAGG	GGAATATATA	CTTCACACNG	420
GGATCTAAC	TTTACTNCA	CTTTGTTAT	TTTTTANAA	CCATTGTNTT	GGGCCAACAA	480
CAATGGNAAT	NCCNCCNCNC	TGGACTAGT				509

## (2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TTTTTTTTTT	TTTTTTTG	CCCCCTCTT	ATAAAAAAC	AGTTACCATT	TTATTTACT	60
TACACATATT	TATTTATAA	TTGGTATTAG	ATATTCAAAA	GGCAGCTTT	AAAATCAAAC	120
TAAATGGAAA	CTGCCTTAGA	TACATAATT	TTAGGAATT	GCTTAAAATC	TGCCTAAAGT	180
GAAAATCTTC	TCTAGCTCTT	TTGACTGTAA	ATTTTGACT	CTTGTAAAAC	ATCCAAATTC	240
ATTTTCTTG	TCTTTAAAAT	TATCTAATCT	TTCCATT	TCCCTATTCC	AAGTCAATT	300
GCTTCTCTAG	CCTCATTCC	TAGCTCTTAT	CTACTATTAG	TAAGTGGCTT	TTTCCTAAA	360
AGGGAAAACA	GGAAGAGANA	ATGGCACACA	AAACAAACAT	TTTATATTCA	TATTTCTACC	420
TACGTTAATA	AAATAGCATT	TTGTGAAGCC	AGCTAAAAG	AAGGCTTAGA	TCCTTTATG	480
TCCATTCTAG	TCACTAAACG	ATATCNAAG	TGCCAGAATG	CAAAAGGTTT	GTGAACATTT	540
ATTCAAAAGC	TAATATAAGA	TATTCACAT	ACTCATCTT	CTG		583

## (2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TTTTTTTTNT	TTTTTTTTTT	TTTTTNCTC	TTCTTTTTT	TTGANAATGA	GGATCGAGTT	60
TTTCACTCTC	TAGATAGGGC	ATGAAGAAAA	CTCATCTTC	CAGCTTAAA	ATAACAATCA	120
AATCTCTTAT	GCTATATCAT	ATTTAAGTT	AAACTAATGA	GTCACTGGCT	TATCTTCTCC	180
TGAAGGAAAT	CTGTTCATTC	TTCTCATTCA	TATAGTTATA	TCAAGTACTA	CCTTGCATAT	240
TGAGAGGTTT	TTCTTCTCTA	TTTACACATA	TATTTCCATG	TGAATTGTA	TCAAACCTTT	300
ATTTTCATGC	AAACTAGAAA	ATAATGTNTT	CTTTGCATA	AGAGAAGAGA	ACAATATNAG	360
CATTACAAAA	CTGCTCAAAT	TGTTGTTAA	GNTTATCCAT	TATAATTAGT	TNGGCAGGAG	420
CTAATACAAA	TCACATTTAC	NGACNAGCAA	TAATAAAACT	GAAGTACCA	TTAAATATCC	480
AAAATAATTA	AAGGAACATT	TTTACGCTGG	GTATAATTAG	CTAATTCACT	TTACAAGCAT	540
TTATTNAGAA	TGAATTCA	TGTTATTATT	CCNTAGCCC	ACACAATGG		589

## (2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TTTTTNTTTT	TTTTTCAGT	AATAATCAGA	ACAATATT	TTTTTATATT	AAAAATT	60
AGAAAAGTGC	CTTACATT	ATAAAAGTT	GTTTCTAAA	GTGATCAGAG	GAATTAGATA	120
TNGTCTTGAA	CACCAATATT	AATTGAGGA	AAATACACCA	AAATACATTA	AGTAAATTAT	180
TTAAGATCAT	AGAGCTTGTA	AGTAAAAGA	TAAAATTGA	CCTCAGAAC	TCTGAGCATT	240
AAAAATCCAC	TATTAGCAA	TAAATTACTA	TGGACTTCTT	GCTTTAATT	TGTGATGAAT	300
ATGGGGTGT	ACTGGTAAAC	CAACACATT	TGAAGGATAC	ATTACTTAGT	GATAGATTCT	360
TATGTA	CTT	TTT	TCT	TTT	TCAATCTT	420
AAGGGGCNGA	NGAAATGAGG	AAGAAAAGAA	AAGGATTACG	CATACTGTT	TTTCTATNGG	480
AAGGATTAGA	TATGTTCC	TTGCCAATAT	TAAAAAATA	ATAATGTTA	CTACTAGTGA	540
AACCC						545

## (2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TTTTTTTTTT TTTTTTAGTC AAGTTCTNA TTTTTATTAT AATTAAAGTC TTGGTCATTT	60
CATTATTAG CTCTGCAACT TACATATTAA AATTAAAGAA ACGTTNTTAG ACAACTGTNA	120
CAATTATCAA ATGTAAGGTG CCATTATTGA GTANATATAT TCCTCCAAGA GTGGATGTGT	180
CCCTTCTCCC ACCAACTAAT GAANCAGCAA CATTAGTTA ATTTTATTAG TAGATNATAC	240
ACTGCTGCAA ACGCTAATT C TCTTCTCCAT CCCCATGTNG ATATTGTGTA TATGTGTGAG	300
TTGGTNAGAA TGCATCANCA ATCTNACAAT CAACAGCAAG ATGAAGCTAG GCNTGGGCTT	360
TCGGTGAAAA TAGACTGTGT CTGTCTGAAT CAAATGATCT GACCTATCCT CGGTGGCAAG	420
AACTCTTCGA ACCGCTTCCT CAAAGGCNGC TGCCACATT GTGGCNTCTN TTGCACTTGT	480
TTCAAAA	487

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 332 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TGAATTGGCT AAAAGACTGC ATTTTANAA CTAGCAACTC TTATTTCTTT CCTTTAAAAAA	60
TACATAGCAT TAAATCCCAA ATCCTATTAA AAGACCTGAC AGCTTGAGAA GGTCACTACT	120
GCATTTATAG GACCTTCTGG TGGTTCTGCT GTTACNTTG AANTCTGACA ATCCTTGANA	180
ATCTTGAT GCAGAGGAGG TAAAAGGTAT TGGATTTCA CAGAGGAANA ACACAGCGCA	240
GAAATGAAGG GGCCAGGCTT ACTGAGCTTG TCCACTGGAG GGCTCATGGG TGGGACATGG	300
AAAAGAAGGC AGCCTAGGCC CTGGGGAGCC CA	332

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 524 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGGGCGTGGT GCGGAGGGCG TTACTGTTTT GTCTCAGTAA CAATAAATAC AAAAAGACTG	60
GTTGTGTTCC GGCCCCATCC AACACAGAAG TTGATTCTC TTGTGTGCAG AGTGAATGAT	120
TTTAAAGGAC ATGGAGCTTG TCACAAATGTC ACAATGTCAC AGTGTGAAGG GCACACTCAC	180
TCCCGCGTGA TTCACATTAA GCAACCAACA ATAGCTCATG AGTCCATACT TGTAAATACT	240
TTTGGCAGAA TACTTNTTGA AACTGCAGA TGATAACTAA GATCCAAGAT ATTTCCAAA	300
GTAAATAGAA GTGGGTCTATA ATATTAATTA CCTGTTCTACA TCAGCTTCCA TTTACAAGTC	360
ATGAGCCCAG AACTGACAT CAAACTAAGC CCACTTAGAC TCCTCACCAAC CAGTCTGTCC	420
TGTCATCAGA CAGGAGGCTG TCACCTTGAC CAAATTCTCA CCAGTCAATC ATCTATCAA	480
AAACCATTAC CTGATCCACT TCCGGTAATG CACCACCTTG GTGA	524

(2) INFORMATION FOR SEQ ID NO:209:

120

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGGTGAGGAA ATCCAGAGTT GCCATGGAGA AAATTCCAGT GTCAGCATTC TTGCTCCTTG	60
TGGCCCTCTC CTACACTCTG GCCAGAGATA CCACAGTCAA ACCTGGAGCC AAAAAGGACA	120
CAAAGGACTC TCGACCCAAA CTGCCCCAGA CCCTCTCCA	159

## (2) INFORMATION FOR SEQ ID NO:210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

ACTCCCTGGC AGACAAAGGC AGAGGGAGAGA GCTCTGTTAG TTCTGTGTTG TTGAAC TGCC	60
ACTGAATTTC TTTCCACTTG GACTATTACA TGCCANTTGA GGGACTAATG GAAAAACGTA	120
TGGGGAGATT TTANCCAATT TANGTNTGTA AATGGGGAGA CTGGGGCAGG CGGGAGAGAT	180
TTGCAGGGTG NAAATGGGAN GGCTGGTTG TTANATGAAC AGGGACATAG GAGGTAGGCA	240
CCAGGATGCT AAATCA	256

## (2) INFORMATION FOR SEQ ID NO:211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ACATTGTTTT TTTGAGATAA AGCATTGAGA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTTAAGGAGA	180
GGGGAGATAC ATTNGAAAG AGGACTGAAA GAAATACTCA AGTNGGAAAA CAGAAAAAGA	240
AAAAAAGGAG CAAATGAGAA GCCT	264

## (2) INFORMATION FOR SEQ ID NO:212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

ACCCAAAAAT CCAATGCTGA ATATTTGGCT TCATTATTCC CANATTCTT GATTGTCAA	60
GGATTAAATG TTGTCTCAGC TTGGGCACTT CAGTTAGGAC CTAAGGATGC CAGCCGGCAG	120
GTTCATATAT GCAGCAACAA TATTCAAGCG CGACAACAGG TTATTGAAC TGCCCGCCAG	180
TTNAATTCA TTCCCATTGA CTTGGGATCC TTATCATCAG CCAGAGAGAT TGAAAATTAA	240
CCCCTACNAC TCTTTACTCT CTGGANAGGG CCAGTGGTGG TAGCTATAAG CTTGGCCACA	300
TTTTTTTTTC CTTTATTCCCT TTGTCAGA	328

## (2) INFORMATION FOR SEQ ID NO:213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ACTTATGAGC AGAGCGACAT ATCCNAGTGT AGACTGAATA AAACTGAATT CTCTCCAGTT	60
TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT	120
CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAAACT TCTTCCTCAT TCCAAGAGTT	180
TTCAATATTT GCATGAACCT GCTGATAANC CATGTTAANA AACAAATATC TCTCTNACCT	240
TCTCATCGGT	250

## (2) INFORMATION FOR SEQ ID NO:214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

ACCCAGAACAT CAATGCTGAA TATTTGGCTT CATTATTCCC AGATTCTTG ATTGTCAAAG	60
GATTAAATGT TGTCTCAGCT TGGGCACTTC AGTTAGGACC TAAGGATGCC AGCCGGCAGG	120
TTTATATATG CAGCAACAAAT ATTCAAGCGC GACAACAGGT TATTGAACCT GCCCGCCAGT	180
TGAATTTCAT TCCCATTGAC TTGGGATCCT TATCATCAGC CANAGAGATT GAAAATTAC	240
CCCTACGACT CTTTACTCTC TGGAGAGGGC CAGTGGTGGT AGCTATAAGC TTGGCCACAT	300
TTTTTTTCC TTTATTCCCT TGTCAGAGAT GCGATTTCATC CATATGCTAN AAACCAACAG	360
AGTGACTTTT ACAAAATTCC TATAGANATT GTGAATAAAA CCTTACCTAT AGTTGCCATT	420
ACTTTGCTCT CCCTAATATA CCTC	444

## (2) INFORMATION FOR SEQ ID NO:215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ACTTATGAGC AGAGCGACAT ATCCAAGTGT ANACTGAATA AAACTGAATT CTCTCCAGTT	60
TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT	120

CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAACT TCTTCCTCAT TCCAAGAGTT	180
TTCAATATTT GCATGAACCT GCTGATAAGC CATGTTGAGA AACAAATATC TCTCTGACCT	240
TCTCATCGGT AAGCAGAGGC TGTAGGCAAC ATGGACCATA GCGAANAAAA AACTTAGTAA	300
TCCAAGCTGT TTTCTACACT GTAACCAGGT TTCCAACCAA GGTGGAAATC TCCTATACTT	360
GGTGCC	366

## (2) INFORMATION FOR SEQ ID NO:216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTGTATAAAC AGAACTCCAC TGCANGAGGG AGGGCCGGGC CAGGAGAATC TCCGCTTGT	60
CAAGACAGGG GCCTAAGGAG GGTCTCCACA CTGCTNNNTAA GGGCTNTTNC ATTTTTTTAT	120
TAATAAAAAG TNNAAAAGGC CTCTTCTCAA CTTTTTCCC TTNGGCTGGA AAATTTAAAA	180
ATCAAAAATT TCCTNAAGTT NTCAAGCTAT CATATATACT NTATCCTGAA AAAGCAACAT	240
AATTCTTCCT TCCCTCCTT	260

## (2) INFORMATION FOR SEQ ID NO:217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG GTAAGTTTAN AAATGTTATA ATTCAGGAA NAGGAACGCA TATAATTGTA	60
TCTTGCTTAT AATTTTCTAT TTTAATAAGG AAATAGCAAA TTGGGGTGGG GGGAAATGTAG	120
GGCATTCTAC AGTTTGAGCA AAATGCAATT AAATGTGGAA GGACAGCACT GAAAAATT	180
ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATTT ATAATTAGCC ACTTACCTA	240
ATATCCTTCA TGCTTGAA GT	262

## (2) INFORMATION FOR SEQ ID NO:218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGGCCAA CCCCTGAGCA	60
CCCCTATCAA CTCCCTTTG TAGTAAACTT GGAACCTTGG AAATGACCAG GCCAAGACTC	120
AGGCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGTNTNA NGTCCAGGGT TGCTAGGAAA	180
ANAAATCAGC AGACACAGGT GTAAA	205

## (2) INFORMATION FOR SEQ ID NO:219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TACTGTTTG TCTCAGTAAC AATAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA	60
ACCACGAAGT TGATTTCTCT TGTGTGCAGA GTGACTGATT TTAAAGGACA TGGA	114

## (2) INFORMATION FOR SEQ ID NO:220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

ACTAGCCAGC ACAAAAGGCA GGGTAGCCTG AATTGCTTTC TGCTCTTAC ATTTCTTTA	60
AAATAAGCAT TTAGTGCTCA GTCCCTACTG AGT	93

## (2) INFORMATION FOR SEQ ID NO:221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ACTANGTGCA GGTGCGCACA AATATTGTC GATATTCCCT TCATCTTGGA TTCCATGAGG	60
TCTTTGCCC AGCCTGTGGC TCTACTGTAG TAAGTTCTG CTGATGAGGA GCCAGNATGC	120
CCCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCCAA CCTCTGT	167

## (2) INFORMATION FOR SEQ ID NO:222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AGGGCGTGGT GCGGAGGGCG GTACTGACCT CATTAGTAGG AGGATGCATT CTGGCACCCC	60
GTTCTTCACC TGTCCCCAA TCCTTAAAG GCCATACTGC ATAAAGTCAA CAACAGATAA	120
ATGTTTGCTG AATTAAAGGA TGGATGAAAA AAATTAATAA TGAATTCTTG CATAATCCAA	180
TTTTCTCTTT TATATTCTA GAAGAAGTTT CTTTGAGCCT ATTAGATCCC GGGAAATCTT	240
TAGGTGAGCA TGATTAGAGA GCTTGTAGGT TGCTTTACA TATATCTGGC ATATTGAGT	300

CTCGTATCAA AACAAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T

351

## (2) INFORMATION FOR SEQ ID NO:223

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAACAAACA AACAAAAAAA ACAATTCTTC ATTCAAGAAAA ATTATCTTAG GGACTGATAT	60
TGGTAATTAT GGTCAATTAA ATWRTRTTGT GGGCATTTC CTTACATTGT CTTGACAAGA	120
TTAAAATGTC TGTGCCAAAA TTTTGTATT TATTTGGAGA CTTCTTATCA AAAGTAATGC	180
TGCCAAAGGA AGTCTAAGGA ATTAGTAGTG TTCCCMTCAC TTGTTGGAG TGTGCTATT	240
TAAAAGATT TGATTTCTG GAATGACAAT TATATTTAA CTTTGGTGGG GGAAANAGTT	300
ATAGGACCAC AGTCTTCACT TCTGATACTT GTAAATTAAT CTTTATTGC ACTTGTGTTG	360
ACCATTAAGC TATATGTTA AAA	383

## (2) INFORMATION FOR SEQ ID NO:224

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

CCCCTGAAGG CTTCTTGTAA GAAAATAGTA CAGTTACAAC CAATAGGAAC AACAAAAAGA	60
AAAAGTTGT GACATTGTAG TAGGGAGTGT GTACCCCTTA CTCCCCATCA AAAAAAAAAT	120
GGATACATGG TTAAAGGATA RAAGGGCAAT ATTTTATCAT ATGTTCTAAA AGAGAAGGAA	180
GAGAAAATAC TACTTCTCR AAATGGAAGC CCTTAAAGGT GCTTGATAC TGAAGGACAC	240
AAATGTGGCC GTCCATCCTC CTTTARAGTT GCATGACTG GACACGGTAA CTGTTGCAGT	300
TTTARACTCM GCATTGTGAC	320

## CLAIMS

1. A polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.
2. A DNA molecule comprising a nucleotide sequence encoding the polypeptide of claim 1.
3. A DNA molecule having a sequence provided in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224.
4. An expression vector comprising the DNA molecule of claims 2 or 3.
5. A host cell transformed with the expression vector of claim 4.
6. The host cell of claim 5 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cell lines.
7. A pharmaceutical composition comprising the polypeptide of claim 1 and a physiologically acceptable carrier.
8. A vaccine comprising the polypeptide of claim 1 and a non-specific immune response enhancer.

9. The vaccine of claim 8 wherein the non-specific immune response enhancer is an adjuvant.

10. A vaccine comprising the DNA molecule of claims 2 or 3 and a non-specific immune response enhancer.

11. The vaccine of claim 10 wherein the non-specific immune response enhancer is an adjuvant.

12. A pharmaceutical composition for the treatment of prostate cancer comprising a polypeptide and a physiologically acceptable carrier, the polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

13. A vaccine for the treatment of prostate cancer comprising a polypeptide and a non-specific immune response enhancer, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences

14. The vaccine of claim 13 wherein the non-specific immune response enhancer is an adjuvant.

15. A vaccine for the treatment of prostate cancer comprising a DNA molecule and a non-specific immune response enhancer, the DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

16. The vaccine of claim 15 wherein the non-specific immune response enhancer is an adjuvant.

17. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claims 7 or 12.

18. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of any one of claims 8, 10, 13 or 15.

19. A fusion protein comprising two or more polypeptides according to claim 1.

20. A fusion protein comprising a polypeptide according to claim 1 and a known prostate antigen.

21. A pharmaceutical composition comprising a fusion protein according to any one of claims 19-20 and a physiologically acceptable carrier.

22. A vaccine comprising a fusion protein according to any one of claims 19-20 and a non-specific immune response enhancer.

23. The vaccine of claim 22 wherein the non-specific immune response enhancer is an adjuvant.

24. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claim 21.

25. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of claim 22.



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification <sup>6</sup> : C12N 15/12, C07K 14/705, C12N 5/10, 1/21, A61K 38/17, C12N 1/19, A61K 39/00, C12N 15/62		A3	(11) International Publication Number: <b>WO 98/37093</b>
			(43) International Publication Date: 27 August 1998 (27.08.98)
(21) International Application Number:	PCT/US98/03492		(81) Designated States: AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).
(22) International Filing Date:	25 February 1998 (25.02.98)		
(30) Priority Data:			
08/806,099	25 February 1997 (25.02.97)	US	
08/904,804	1 August 1997 (01.08.97)	US	
09/020,956	9 February 1998 (09.02.98)	US	
(71) Applicant:	CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).		
(72) Inventors:	XU, Jiangchun; 15805 Southeast 43rd Place, Bellevue, WA 98006 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US).		
(74) Agents:	MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).		
			(88) Date of publication of the international search report: 17 December 1998 (17.12.98)

(54) Title: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE

## (57) Abstract

Compounds and methods for treating prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of prostate cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides.

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DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		

# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/US 98/03492

A. CLASSIFICATION OF SUBJECT MATTER					
IPC 6	C12N15/12	C07K14/705	C12N5/10	C12N1/21	A61K38/17
	C12N1/19	A61K39/00	C12N15/62		

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K C12N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 95 04548 A (JENNER TECHNOLOGIES) 16 February 1995 see the whole document ---	
A	WO 93 25224 A (VETROGEN CORP) 23 December 1993 see the whole document ---	
A	WO 95 30758 A (MAYO FOUNDATION ;HYBRITECH INC (US); TINDALL DONALD J (US); YOUNG) 16 November 1995 see the whole document ---	
A	EP 0 652 014 A (NAT INST IMMUNOLOGY) 10 May 1995 see the whole document ---	
		-/-

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

\* Special categories of cited documents :

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- \*E\* earlier document but published on or after the international filing date
- \*L\* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- \*O\* document referring to an oral disclosure, use, exhibition or other means
- \*P\* document published prior to the international filing date but later than the priority date claimed

- \*T\* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- \*X\* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- \*Y\* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- \*&\* document member of the same patent family

Date of the actual completion of the international search

30 July 1998

Date of mailing of the international search report

03.11.1998

Name and mailing address of the ISA

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Fax: (+31-70) 340-3016

Authorized officer

Oderwald, H

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/03492

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>SHORT J M ET AL: "LAMBDA ZAP: A BACTERIOPHAGE LAMBDA EXPRESSION VECTOR WITH IN VIVO EXCISION PROPERTIES" NUCLEIC ACIDS RESEARCH, vol. 16, no. 15, 1988, pages 7583-7600, XP002007597 see the whole document &amp; "AC No. AA453562" EMBL SEQUENCE DATABASE, 10 May 1990, HEIDELBERG, GERMANY, see nucleotides 398-765</p> <p>---</p>	2,4-6
X,P	<p>HILLIER L ET AL: "Homo sapiens cDNA clone 788180 (AC No. AA453562)" EMBL SEQUENCE DATABASE, 11 June 1997, HEIDELBERG, GERMANY, XP002073072 see the whole document</p> <p>-----</p>	2,4-6

# INTERNATIONAL SEARCH REPORT

Int. application No.

PCT/US 98/03492

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1.  Claims Nos.:

because they relate to subject matter not required to be searched by this Authority, namely:

Remark: Although claims 17, 18, 24 and 25 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

2.  Claims Nos.:

because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3.  Claims Nos.:

because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see further information sheet

1.  As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2.  As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3.  As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4.  No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see further information sheet, subject 1.

### Remark on Protest

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-11 and 17-25 all partially

A polypeptide comprising an immunogenic portion or a variant of a prostate protein encoded by SEQ ID NO:2, DNA molecules related to said protein, expression vectors comprising said DNA molecules, hosts transformed with said vectors, fusion proteins comprising said polypeptide, pharmaceutical compositions and vaccines comprising said polypeptide, fusion proteins and DNA.

2. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 3.

3. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 8.

4. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 9.

5. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 10.

6. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 11.

7. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 12.

8. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 13.

9. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 14.

10. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 15.

11. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 16.

12. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 17.

13. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 18.

14. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 19.

15. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 20.

16. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 21.

17. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 22.

18. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 23.

19. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 24.

20. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 25.

21. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 26.

22. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 27.

23. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 28.

24. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 29.

25. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 41.

26. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 42.

27. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 43.

28. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 44.

29. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 45.

30. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 47.

31. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 48.

32. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 49.

33. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 50.

34. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 51.

35. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 52.

36. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 54.

37. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 55.

38. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 56.

39. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 57.

40. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 58.

41. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 59.

42. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 60.

43. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 61.

44. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 62.

45. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 63.

46. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 64.

47. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 65.

48. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 70.

49. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 73.

50. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 74.

51. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 79.

52. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 81.

53. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 87.

54. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 90.

55. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 92.

56. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 93.

57. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 97.

58. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 103.

59. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 104.

60. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 107.

61. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 109.

62. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 110.

63. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 111.

64. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 115.

65. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 116.

66. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 117.

67. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 118.

68. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 119.

69. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 120.

70. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 121.

71. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 122.

72. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 123.

73. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 124.

74. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 125.

75. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 126.

76. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 127.

77. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 128.

78. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 129.

79. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 130.

80. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 131.

81. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 132.

82. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 133.

83. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 134.

84. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 135.

85. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 136.

86. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 137.

87. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 138.

88. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 139.

89. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 140.

90. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 141.

91. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 142.

92. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 143.

93. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 144.

94. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 145.

95. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 146.

96. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 147.

97. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 148.

98. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 149.

99. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 150.

100. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 151.

101. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 152

102. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 153.

103. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 154.

104. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 155.

105. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 156.

106. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 157.

107. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 158.

108. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 159.

109. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 160.

110. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 171.

111. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 173.

112. Claims: 1-11 and 17-25  
same as invention 1 but for SEQ ID NO: 174.

113. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 175.

114. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 177.

115. Claims: 1-11 and 17-25  
same as invention 1 but for SEQ ID NO: 181.

116. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 188.

117. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 191.

118. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 193.

119. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 194.

120. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 198.

121. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 203.

122. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 204.

123. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 207.

124. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 209.

125. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 210.

126. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 211.

127. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 220.

128. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 222.

129. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 223.

130. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 224.

131. Claims: 12-18 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Pharmaceutical compositions and a vaccines comprising an immunogenic portion or a variant of a prostate-specific polypeptide and related DNA sequences, said DNA sequences recited in SEQ ID NO: 5.

132. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 6.
133. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 7.
134. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 30.
135. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 31.
136. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 32.
137. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 33.
138. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 34.
139. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 35.
140. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 36.
141. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 37.

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142. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 38.

143. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 39.

144. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 40.

145. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 46.

146. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 53.

147. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 66.

148. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 67.

149. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 68.

150. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 69.

151. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 71.

152. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 72.

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153. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 75.

154. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 76.

155. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 77.

156. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 78.

157. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 80.

158. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 82.

159. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 83.

160. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 84.

161. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 85.

162. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 86.

163. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 88.

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164. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 89.
165. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 91.
166. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 94.
167. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 95.
168. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 96.
169. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 98.
170. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 99.
171. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 100.
172. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 101.
173. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 102.
174. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 105.

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175. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 106.
176. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 161.
177. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 162.
178. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 163.
179. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 164.
180. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 165.
181. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 166.
182. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 167.
183. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 168.
184. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 169.
185. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 170.

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186. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 179.

187. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 180.

188. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 182.

189. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 183.

190. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 184.

191. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 185.

192. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 186.

193. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 187.

194. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 189.

195. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 190.

196. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 192.

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197. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 195.
198. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 196.
199. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 197.
200. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 199.
201. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 200.
202. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 201.
203. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 202.
204. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 205.
205. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 206.
206. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 208.
207. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 212.

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208. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 213.

209. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 214.

210. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 215.

211. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 216.

212. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 217.

213. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 218.

214. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 219.

215. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 221.

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